

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 07:35:55 ; Search time 131 Seconds
(without alignments)
2122.369 Million cell updates/sec

Title: US-10-014-101-4
Perfect score: 2596
Sequence: 1 MANLRMLITLITVLMITKSS.....SKRKDLDPKLLSPGQDIF 501

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10014101/runat_05042004_154155_8600/app_query.fasta_1.647
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	44.0	1605	3	US-09-124-541-3 Sequence 3, Appli
2	1141	44.0	1605	4	US-09-663-326-3 Sequence 3, Appli
3	1014	39.1	6733	3	US-09-124-541-2 Sequence 2, Appli
4	1014	39.1	6733	4	US-09-663-326-2 Sequence 2, Appli
5	835	32.2	1602	3	US-09-124-541-10 Sequence 10, Appl
6	835	32.2	1602	4	US-09-663-326-10 Sequence 10, Appl
7	198.5	7.6	4403765	3	US-09-103-840A-2 Sequence 2, Appli
8	196.5	7.6	4411529	3	US-09-103-840A-1 Sequence 1, Appli
9	183.5	7.1	37769	4	US-08-311-731A-23 Sequence 23, Appl
10	178	6.9	1419	4	US-09-266-965-61 Sequence 61, Appl
11	178	6.9	53500	4	US-09-266-965-76 Sequence 76, Appl
12	177.5	6.8	1833	4	US-09-630-983A-2 Sequence 2, Appli

13	175.5	6.8	2034	4	US-09-423-468A-12 Sequence 12, Appl
14	175.5	6.8	2064	4	US-09-630-983A-4 Sequence 4, Appli
15	174	6.7	1407	4	US-09-328-352-1897 Sequence 1897, Ap
16	171.5	6.6	1553	3	US-09-217-490-1 Sequence 1, Appli
17	169	6.5	2120	4	US-09-630-983A-10 Sequence 10, Appl
18	168.5	6.5	1981	4	US-09-647-390-17 Sequence 17, Appl
19	166	6.4	3111	4	US-09-489-039A-3095 Sequence 3095, Ap
20	160	6.2	3060	4	US-09-543-681A-275 Sequence 275, App
21	155.5	6.0	3680	4	US-09-647-390-15 Sequence 15, Appl
22	153.5	5.9	1474	4	US-08-624-447-1 Sequence 1, Appli
23	150.5	5.8	1365	4	US-09-894-844-73 Sequence 73, Appl
24	150.5	5.8	4403765	3	US-09-103-840A-2 Sequence 2, Appli
25	150.5	5.8	4411529	3	US-09-103-840A-1 Sequence 1, Appli
26	146.5	5.6	1545	4	US-09-266-965-31 Sequence 31, Appl
27	146.5	5.6	18331	4	US-09-266-965-96 Sequence 96, Appl
28	146.5	5.6	53500	4	US-09-266-965-76 Sequence 76, Appl
29	142.5	5.5	1809	4	US-09-589-733C-5 Sequence 5, Appli
30	138.5	5.3	1830121	4	US-09-557-884-1 Sequence 1, Appli
31	138.5	5.3	1830121	4	US-09-643-990A-1 Sequence 1, Appli
32	133	5.1	2169	5	PCT-US96-05320A-264 Sequence 264, App
33	133	5.1	1830121	4	US-09-557-884-1 Sequence 1, Appli
34	133	5.1	1830121	4	US-09-643-990A-1 Sequence 1, Appli
35	132	5.1	1284	4	US-09-894-844-106 Sequence 106, App
36	129.5	5.0	1581	4	US-09-630-983A-6 Sequence 6, Appli
37	129.5	5.0	2138	4	US-09-630-983A-8 Sequence 8, Appli
38	127	4.9	99629	4	US-09-596-002-37 Sequence 37, Appl
39	126.5	4.9	1392	4	US-09-252-991A-7430 Sequence 7430, Ap
40	126.5	4.9	1932	4	US-09-252-991A-7271 Sequence 7271, Ap
41	126	4.9	1422	4	US-09-540-236-1736 Sequence 1736, Ap
42	116	4.5	1509	4	US-09-252-991A-11048 Sequence 11048, A
43	116	4.5	1590	4	US-09-252-991A-11206 Sequence 11206, A
44	116	4.5	4061	3	US-08-425-843-1 Sequence 1, Appli
45	115	4.4	1467	4	US-09-540-236-761 Sequence 761, App

ALIGNMENTS

RESULT 1
US-09-124-541-3
; Sequence 3, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-124-541-3

Alignment Scores:			
Pred. No.:	6.23e-132	Length:	1605
Score:	1141.00	Matches:	233
Percent Similarity:	63.71%	Conservative:	83
Best Local Similarity:	46.98%	Mismatches:	152
Query Match:	43.95%	Indels:	28
DB:	3	Gaps:	11

US-10-014-101-4 (1-501) x US-09-124-541-3 (1-1605)

Qy 30 SerLeuAsnLeuThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPhe 49
Db 124 GCCTTGGACGGCAAGCTCCGGACCGACAGCAACGCGGCGGCTTCGACGGACTTC 183

QY 50 GlyAsnIleThrThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIle 69
Db 184 GGCAACATCATCGTGGCGCTCCCGCGGCTCTGTACCGTCTGTCCACGGCGACCTG 243
QY 70 SerArgLeuLeuGlnTyrAlaAlaAsnGlyLysSer-----ThrPheGlnValAlaAla 87
Db 244 GTGGCGCTGCTGAGC---GCGGCCAACTCCACCCCGGGGTGGCCCTACACCATCGCGTTC 300
QY 88 ArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsn 107
Db 301 CGCGCGCGCGCCACTCCCTCATGGGCCAGGCCCTTCGCCCCCGCGCGCTGCTCGTCAAC 360
QY 108 MetThrCysIleThrAsp-----ValValValSerLysAspLysLys 121
Db 361 ATGGCGTCCCTGGGCGACGCGCGCGCGCGCGCGCGCGCATCAACGTGTCCGCGGACGGCGCG 420
QY 122 TyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGluLys 141
Db 421 TACGTGGACCGCGCGCGAGCAGGTGTGGATCGACGTGTTCGCGCGCTCGCTGGCGCGC 480
QY 142 GlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSer 161
Db 481 GCGGTGGCGCGCGCTCCTTGGAAAGCACTACCTTACCTACCGTTCGCGCGCGCATCGTGTCC 540
QY 162 AsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGlu 181
Db 541 AACGCAGGCATCAGCGGCCAGCGGTTCGCGCCACGCGCCACAGATATCTAACGTCTGGAG 600
QY 182 LeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGlu 201
Db 601 ATGGACGTATACCGGCCCATGGGAGATGGTGACGTGTCTCAAGCAGCTGAACCGCGAC 660
QY 202 LeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIle 221
Db 661 CTGTTTCGACGCGCTCTGGCGGGCTGGGCGAGTTCGGAGTGATCACCCGGCGCGCGATC 720
QY 222 ValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThr 241
Db 721 GCGGTGGAGCGCGCGCGCGCGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
QY 242 ThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGly----- 258
Db 781 GCGTTTCAGCGCGCACGAGGCGGTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 259 -----ValAspTyrLeuGluGlyGlnIlePhe-----LeuSerAsnGly 271
Db 841 TTCGGCCCGATAGCTACGTGGAAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
QY 272 ValValAspThrSerPhePheProProSerAspGlnSerLysValAlaAspLeuValLys 291
Db 901 CTGGCGAACACGGGGTCTTCCACCGACGCGACGCTCGCCGGATCGTCCGCTCGCGCGG 960
QY 292 GlnHisGly-----IleIleTyrValLeuGluValAlaLysTyrTyrAspProAsn 309
Db 961 GAGCGGAACGCCACCCACCGTGTACAGCATCGAGGCCACGCTCAACTACGACAACGCCACG 1020
QY 310 -----LeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSerTyrLeu 327
Db 1021 GCGGCGCGCGCGCGCGGTGGACAGGCTCGCGTCCGTGGTGGTGGTGGTGGTGGTGGTGG 1080
QY 328 ProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgValHisVal 347
Db 1081 GAGGGGTTCGCGTTCACAGCGCGACGTGGCCCTACCGCGCGTTCCTTGACCGGGTGACCGC 1140
QY 348 GluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeu 367
Db 1141 GAGGAGGTGGCGCTCAACAAGCTGGGGCTGTGGCGGGTGGCGCACCCCGTGGCTCAACATG 1200
QY 368 TyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeu 387
Db 1201 TTCGTGCGCGCTCGCGGATCGCCGACTTCGACCCGCGCGGTGTTCGAAGGCGCATC---CTG 1257

QY 388 LysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAsp 407
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QY 408 AsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIleGlyLeu 427
Db 1318 GACGGCATGTGGCGCGCGACGCG-----TCTGAGGACGTGTCTACCGCGTGTGCTG 1371
QY 428 Leu---GlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluLysIle 446
Db 1372 CTCTTCTCGTGGTGGCGGCCAACGACCTGGCGGAGGCTGCAGGAGCAGAACAGGAGGATC 1431
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Db 1432 CTGCGCTTCTGCGACCTCGCGGGGATCCAGTACAAGACCTACCTGGCGCGGCACACGGAC 1491
QY 467 LysGluAspTrpIleGluHisPheGly---SerLysTrpAspPheSerLysArgLys 485
Db 1492 CGAGTGAAGTGGTCCGCCCACTTCGGCGCGCGCCCAAGTGAATCGCTTCGTGGAGATGAAG 1551
QY 486 AspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1552 AACAAGTACGACCCCAAGAGGTGCTCTCCCCCGGCGCAGGACATCTTC 1599

RESULT 2

US-09-663-326-3
; Sequence 3, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-663-326-3

Alignment Scores:
Pred. No.: 6,23e-132 Length: 1605
Score: 1141.00 Matches: 233
Percent Similarity: 63.71% Conservative: 83
Best Local Similarity: 46.98% Mismatches: 152
Query Match: 43.95% Indels: 28
DB: 4 Gaps: 11

US-10-014-101-4 (1-501) x US-09-663-326-3 (1-1605)

QY 30 SerLeuAsnLeuThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPhe 49
Db 124 GCCTTGGACGGCAAGCTCCGACCGACAGCAACGCGCGCGCGCGCTCGACGACTTC 183
QY 50 GlyAsnIleThrThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIle 69
Db 184 GGCAACATCATCGTGGCGCTCCCGCGCGGTCTGTACCCGTCTGTCACCGGCGGACCTG 243
QY 70 SerArgLeuLeuGlnTyrAlaAlaAsnGlyLysSer-----ThrPheGlnValAlaAla 87
Db 244 GTGGCGCTGCTGAGC---GCGGCCAACTCCACCCCGGGGTGGCCCTACACCATCGCGTTC 300
QY 88 ArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsn 107
Db 301 CGCGCGCGCGCGCATCCTCCTCATGGCGCAGGCTTCGCCCGCGCGGTCTCGTCAAC 360

QY	477	ystrpaspAsppheSerLysArgLysAspLeupheAspProLysLysLeuLeuSerProG	497	OTHER INFORMATION: a,g,c or t
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Dd	3528	AGTGGATCGCTTCGTGGAGATGAAGAACAAGTACGACCCCAAGAGGCTGCTCTCCCCCG	3587	NAME/KEY: variation
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Dd	3588	GCCAGGACATCTTC	3601	LOCATION: (60)
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NAME/KEY: variation
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NAME/KEY: variation
LOCATION: (234)
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NAME/KEY: variation
LOCATION: (237)
OTHER INFORMATION: a,g,c or t

Alignment Scores:
Pred. No.: 9.87e-94 Length: 1602
Score: 835.00 Matches: 186
Percent Similarity: 48.99% Conservative: 56
Best Local Similarity: 37.65% Mismatches: 214
Query Match: 32.16% Indels: 38
DB: 4 Gaps: 13

US-10-014-101-4 (1-501) x US-09-663-326-10 (1-1602)

QY 37 ThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThr 56
Db 145 ACNGAYWSNAAYGCNACNGCNGCNGCNGACNGAYTTYGGNAAAYATHACNWSNGCNYTN 204
QY 57 ProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAla 76
Db 205 CCNGCNGCNGTNTYTAYCCNWSNWSNACNGNGAY--YTNGTNGCNYTNTYTNWSNGCN 261
QY 77 AlaAsnGlyLysSer-----ThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeu 94
Db 262 GCNAAAYWSNACNCCNGGNTGGCCNTAYACNATHGCNTTYMGNGGNGMNGNCAYWSNYTN 321
QY 95 AsnGlyGlnAlaSerValSerGlyValIleValAsnMetThrCysIleThrAsp--- 113
Db 322 ATGGGNCARGCNTTYGCNCCNGGNGGNGTNGTNGTNAAYATGGCNWSNYTNGNGAYGCN 381
QY 114 -----ValValValSerLysAspLysLysTyrAlaAspValAlaAlaGly 128
Db 382 GCNGCNCNCCNMGNATHAAYGTNWSNGCNGAYGGNMGTAYGTNGAYCGNGGNGGAR 441
QY 129 ThrLeuTyrValAspValLeuLysLysThrAlaGluLysGlyValSerProValSerTyr 148
Db 442 CARGTNTGGATHGAYGTNTYTMGNGCNWSNYTNGCNGGNGTNGCNCNMGNWSNTGG 501
QY 149 ThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGln 168
Db 502 AAYGAYTAYTNTAYTNAACNGTNGGNGGNCACNYTNWSNAAAYCGCNGGNATHWSNGNCAR 561
QY 169 ValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLys 188
Db 562 GCNTTYMGNCAYGGNCCNCARATHWSNAAAYGTNTYTNGARATGGAYGTNATHACNGNCAY 621
QY 189 GlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGly 208
Db 622 GNGARATGGTNAACNTGYWSNAARCAARYTNAAYGCNGAYTYTNTTYGAYCGNGTNTYTNNGN 681
QY 209 GlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLys 228
Db 682 GGNYTNGNCARTTYGGNGTNAHACNMGNCNMGNATHGCGNGTNGARCCNGCNCNGCN 741
QY 229 ArgAlaLysTyrPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGlu 248
Db 742 MCGNCNMGNTGGTNGMGTNTYGTNTAYACNGAYTTYGCNGCNTTYWSNGCNGAYCARGAR 801
QY 249 ArgLeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeu 262
Db 802 MGNYTNAACNCCNMGNCCNGGNGGNGGNGCNGWSNTTYGNCNCNATGWSNTAYGTN 861
QY 263 GluGlyGlnIlePheLeu-----SerAsnGlyValValAspThrSerPhePhe 278

Db 862 GARGGNWSNGTNTTYGTNAAYCARWSNYTNGCNACNGAYTYTNGCNAAAYACNGGNTTYTYT 921
QY 279 ProProSerAspGlnSerLysValAlaAspLeuValLysGlnHisGly----- 294
Db 922 ACNGAYGCNGAY-----GTNGCNMGNATHGTNGCNYTNGCNGNGARMGNAAYGCN 972
QY 295 ---IleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsnLeuProIlelle 313
Db 973 ACNACNGTNTAYWSNATHGARGCNACNYTNAAYTAYGAY-----AAYGCNACNGCNGCN 1026
QY 314 SerLysValIleAsp-----ThreLeuThrLysThrLeuSerTyrLeuProGly 329
Db 1027 GCNGCNGCNGTNGAYCARGARYTNGCNWSNGTNYTNGNACNYTNGSNTAYGTNGARGGN 1086
QY 330 PheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGlu 349
Db 1087 TTYGCNTTYCARMGNGAYGTNGCNTAYGCNGCNTTYTNGAYMGNGTNCAYGGNGARGAR 1146
QY 350 AsnLysLeuArgSerIleuGlyLeuTyrPgluLeuProHisProTyrPheAsnLeuTyrVal 369
Db 1147 GTNGCNYTNAAYARYTNGGNYTNTGGMNGTNCNCAYCCNTGGYTNAAYATGTTYGTN 1206
QY 370 ProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGln 389
Db 1207 CCNMGNSNMGNATHGCGAYTTYGAYMNGNGTNTTYAARGGNATH---YTNCARGGN 1263
QY 390 LysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTyrAspAsnArg 409
Db 1264 ACNGAYATHGTNGGNCNCCNYTNGTNTAYCCNYTNAAYARWSNATGTGGAYGAYGCN 1323
QY 410 MetSerAlaMetIleProGluIleAspGluAspValIleTyr---IleIleGlyLeuLeu 428
Db 1324 ATGWSNGCNGCNACNCCN-----WSNGARGAYGTNTTYTAYGCNGTNSNYTNTTY 1377
QY 429 GlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluLysIleArg 448
Db 1378 WSNWSNGTNGCNCNCCNAYGAYTYTNGCNGMGNNTNCARGARCARAAAYMGNMGNATHYTNGN 1437
QY 449 PheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSerLysGlu 468
Db 1438 TTYTGYGAYTYTNGCNGNATHCARTAYAAACNTAYTYTNGCNGMGNCCAYACNGAYMGNWSN 1497
QY 469 AspTyrIleGluHisPheGly---SerLysTyrAspAspPheSerLysArgLysAspLeu 487
Db 1498 GAYTGGTNGMNCAYTTYGGNGCNGCNAARTGGAAYMGNNTTYGTNGARATGAARAAYAR 1557
QY 488 PheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1558 TAYGAYCCNAARMGNTNTYTNWSNCCNGGNCARGAYATHTY 1599

RESULT 7
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence

OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
Alignment Scores: 3.04e-08 Length: 4403765
Pred. No.: 198.50 Matches: 71
Score: 198.50
Percent Similarity: 40.67% Conservative: 38
Best Local Similarity: 26.49% Mismatches: 124
Query Match: 7.65% Indels: 35
DB: 3 Gaps: 6

US-10-014-101-4 (1-501) x US-09-103-840A-2 (1-4403765)
QY 57 ProGlyGlyValIleCysProSerSerThrAla-----AspIleSer 70
Db 4154512 CCGGACTCCTTCGTTGTGATTGCTGCACCCCGCCGACCCCGGATGCAGGGCGAGTTGTCG 4154571
QY 71 ArgLeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAla---AlaArgGly 89
Db 4154572 AGGACTAGGGTATATGCGGTGCCTGTCCCTGGATCTGCACAGTCGGCTTACGCCTGCCGC 4154631
QY 90 GlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMet--- 108
Db 4154632 GTCGAGCGGTTGCTGCGGAGCTATCGATCCATCCCGCGCGACTGCATCCATCCGGCTTGCC 4154691
QY 108 ----- 108

Db 4154692 AAGCCACCTCAAAATCTGTTCGCGCCCGCTCAAAACACGATGCACGGCGCTGGACGCA 4154751
QY 109 ThrCysIleThrAspValVal---ValSerLysAspLysLysTyrAlaAspValAlaAla 127
Db 4154752 TCGGACTGACCGGTGTCATCGGTATCGATCCCGGAGCCCGCACCCGCGACGTCGGCGGC 4154811
QY 128 GlyThrLeuTyrValAspValLeuLysLysThrAlaGluLysGlyValSerProValSer 147
Db 4154812 ATGTGCACATACGAGGACCTAATCGCCGCGACACTGCATACGGTCTGTCCATTTGGTG 4154871
QY 148 ThrThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGly 167
Db 4154872 GTTCCGAGCTGAGGACGATCACATTTGGCGGAGCGGTACCGGCTTGGGTATCGAGTCG 4154931
QY 168 GlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly 187
Db 4154932 GCGTCTGTTCCGCAACGCGCTGCCCCACGAGTCGCTGCTGGAGATGGATATCTCTACCGGC 4154991
QY 188 LysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeu 207
Db 4154992 GCAGGAGAACTTCTCACCGTCTGCCCCGACGACACTCCGACTGTACCGTGATTCCT 4155051
QY 208 GlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaPro 227
Db 4155052 AACTCGTATGGGACACTGGGCTATTCAACCCGGCTTCGAATCCAGCTGGAGCCGCTCCG 4155111
QY 228 LysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGln 247
Db 4155112 CCGTTTGTCCGCTGCGGCACATCCGATTTAGCTCGTTGACGGCGATGGTGGCCGCAATG 4155171
QY 248 GluArgLeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGln 265
Db 4155172 GAGCGCATCATCGACACCGCGGAGTGGACGGGAATCGGTGGACTATCTCGACGGGGTG 4155231
QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProSerAspGlnSerLys 285
Db 4155232 GTTTTCAGCGCT-----GACGAAAGTACCTGTGTCATCGGCATGCAGACGAGC 4155279
QY 286 ValAlaAspLeuValLysGlnHis 293
Db 4155280 GTACCGGGCCCGGTGACGCGACTAC 4155303

RESULT 8
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328

QY 210 LeuGlyGlnPheGlyIleThrArgAlaArgIleValLeuAspHisAlaProLysArg 229
Db 34322 TATGGTACGTTAGGATATTCAACACGGTTTCGGATCTCCCTGGAACTGTAAACCCCTTT 34381
QY 230 AlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArg 249
Db 34382 GTAGCACTGCGACACATCCGATTTCATTGTTGACCGAGATGGTCAACGGCGATGGAAC 34441
QY 250 LeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGlnIlePhe 267
Db 34442 ATCATCGACACCGCGGACACGATGGCGTCCCACTCGATTATCTGGACGGTGTGGTGTTC 34501
QY 268 LeuSerAsn-----GlyValValAspThrSerPhePheProProSer 281
Db 34502 AGTGCTAACGAAAGCTACCTATGCATCGGTAAACGGACCAACACCCCGGACCTGTTCAGC 34561
QY 282 Asp 282
Db 34562 GAC 34564

RESULT 10
US-09-266-965-61
; Sequence 61, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-266-965-61

Alignment Scores:
Pred. No.: 8.37e-12 Length: 1419
Score: 178.00 Matches: 50
Percent Similarity: 50.00% Conservative: 35
Best Local Similarity: 29.41% Mismatches: 73
Query Match: 6.86% Indels: 12
DB: 4 Gaps: 5
US-10-014-101-4 (1-501) x US-09-266-965-61 (1-1419)
QY 57 ProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAla 76
Db 160 CCCGCCCTCGTCGTGTCGCCACCGGTGCGCGGATGTCATCGCCCGCGTTCGCC 219
QY 77 ---AlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsn 95
Db 220 AGGCCCGGGC-----CTTGGATCGCGTCCAGGCCACCGGTAC----- 261
QY 96 GlyGlnAlaSerValSerGlyValIleValAsnMetThrCysIleThrAspValVal 115
Db 262 GGAAGTCTCGCGGCCACCGACCGTCTCATCAGCACCCCGCGGATGACCGCGTCAGG 321
QY 116 ValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeu 135
Db 322 GTCGACCCCGCGGCCGACCGCCCGGATCGAGGCGGGCGTGCCTGGAGCAGGTGATC 381

QY 136 LysLysThrAlaGluLysGlyValSerProValSerTrpThrAspTyrLeuHisIleThr 155
Db 382 CACGAGCGCGCGGCACGGTCTTGACACCGTACCGGCTCGGCCCGTTC----- 432
QY 156 ValGlyGlyThr-----LeuSerAsnGlyGlyIleGlyGlnValPheArgAsnGly 173
Db 433 GTCGCGCGGTCTCTACCTCTCGCGCGCGGCTCGGGCTTCTGTCTCGCGAAGTACGGG 492
QY 174 ProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGlyGluMetLeuThr 193
Db 493 TTCGCGCGGACCATGTCGTCTCGCTCGACCTGGTACGCGCGCGGCGGTTCCTCCAG 552
QY 194 CysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPhe 213
Db 553 GTCTCCGCGGAGGAACACCCCGATCTTCTTGGGCGGTGCGCGGACGAGGGGAACCTC 612
QY 214 GlyIleIleThrArgAlaArgIleValLeu 223
Db 613 GGCATCGTCACCTCCGTCGAGGTGCGGCTG 642

RESULT 11
US-09-266-965-76/c
; Sequence 76, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 53500
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-266-965-76

Alignment Scores:
Pred. No.: 4.84e-09 Length: 53500
Score: 178.00 Matches: 50
Percent Similarity: 50.00% Conservative: 35
Best Local Similarity: 29.41% Mismatches: 73
Query Match: 6.86% Indels: 12
DB: 4 Gaps: 5
US-10-014-101-4 (1-501) x US-09-266-965-76 (1-53500)
QY 57 ProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAla 76
Db 36540 CCCGCCCTCGTCGTGTCGCCACCGGTGCGCGGATGTCATCGCCCGCGTTCGCC 36481
QY 77 ---AlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsn 95
Db 36480 AGGCCCGGGC-----CTTGGATCGCGTCCAGGCCACCGGTAC----- 36439
QY 96 GlyGlnAlaSerValSerGlyValIleValAsnMetThrCysIleThrAspValVal 115
Db 36438 GGAAGTCTCGCGGCCACCGACCGTCTCATCAGCACCCCGCGGATGACCGCGTCAGG 36379
QY 116 ValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeu 135

Db 36378 GTCGACCCGGGGCCCGACCGCCCGGATCGAGGGGGCGGTGGCTGGGAGCAGGTGATC 36319
QY 136 LysLysThrAlaGluLysGlyValSerProValSerTyrThrAspTyrLeuHisIleThr 155
Db 36318 CACGAGCGGGCGGCACGGTCTTGACCGCTGAGCGGCTCGGCGCCGTTCTC----- 36268
QY 156 ValGlyGlyThr-----LeuSerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGly 173
Db 36267 GTCGGCGCGGTCTCCTACCTCCTCGGCGGGGGCTCGGGCTTCTGTCGCGGAAGTACGGG 36208
QY 174 ProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGlyGluMetLeuThr 193
Db 36207 TTCGCCGGCGACCATGTCGTCTCGCTCGACCTGGTGACGGCCGCGGGCGGTTTCTCCAG 36148
QY 194 CysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPhe 213
Db 36147 GTCTCCGGCGAGGAACACCCCGATCTCTTCTGGGCGGTGCGCGGCACGAGGGGAACCTC 36088
QY 214 GlyIleIleThrArgAlaArgIleValLeu 223
Db 36087 GGCATCGTCACCTCCGTCGAGGTCTGGGCTG 36058

RESULT 12
US-09-630-983A-2
; Sequence 2, Application US/09630983A
; Patent No. 6630330
; GENERAL INFORMATION:
; APPLICANT: Porro, Danilo
; APPLICANT: Sauer, Michael
; TITLE OF INVENTION: Ascorbic Acid Production from Yeast
; FILE REFERENCE: 2028.594000
; CURRENT APPLICATION NUMBER: US/09/630,983A
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1833
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A. thaliana
US-09-630-983A-2

Alignment Scores:
Pred. No.: 1.51e-11 Length: 1833
Score: 177.50 Matches: 97
Percent Similarity: 37.23% Conservative: 91
Best Local Similarity: 19.21% Mismatches: 208
Query Match: 6.84% Indels: 109
DB: 4 Gaps: 19

US-10-014-101-4 (1-501) x US-09-630-983A-2 (1-1833)
QY 63 ProSerSerThrAlaAspIleSerArgLeuGlnTyrAlaAlaAsnGlyLysSerThr 82
Db 385 CCGGAGAATCTTGCTGATCTCGAAGCTCTTGTAAAGGAATCTCATGAGAAGAAG----- 438
QY 83 PheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGly 102
Db 439 TTAAGGATTCGTCGCCGTTGGATCGGGTCTCTCGCCTAATGGG---ATTGGTTTGTCTCGC 495
QY 103 GlyValIleValAsnMetThrCysIleThrAspValVal---ValSerLysAspLysLys 121
Db 496 TCTGGGATGGTGAATCTGGCGCTTATGGATAAAGTTCTAGAGGTGGATAAAGAGAAGAAG 555
QY 122 TyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLys 141
Db 556 AGAGTTACGGTCAGGCTGGGATTAGGGTCCAGCAATTTGGTTGACGCCCATTAAGACTAT 615
QY 142 GlyValSerProValSerTyrThrAspTyrLeuHisIleThrValGlyGlyThrLeuSer 161
Db 616 GGTCTTACTTTCAGAACTTTGCCCTCCATTAGAGAGCAGCATTTGGTGTATTATTTCAG 675

QY 162 AsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGlu 181
Db 676 GTTGGGGCACATGGGACAGGTGCT---AGATTGCTCTCTATTGATGAGCAGGTGATCAGT 732
QY 182 LeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGlu 201
Db 733 ATGAAGCTGGTTACTCTCTCGAAGGGAAACAATTGAACTTTCAAGAGAGAAAGATCCGGAG 792
QY 202 LeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIle 221
Db 793 CTCTTTTCATCTAGCTCGATGTGGCCTTGTGGACTTGGAGTTGTT-----GCTGAGGTC 846
QY 222 ValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThr 241
Db 847 ACCCTCCAATGCGTTGCAAGACATGAACTTGTGGAACACACATACGTCTCAAACTTGCAA 906
QY 242 ThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAsp-----Ile 257
Db 907 GAAATCAAGAAAAATCACAAAAAATTGCTCTCT---GCAAAACAAGCATGTTAAGTACCTA 963
QY 258 GlyValAspTyrLeuGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhe 277
Db 964 TATATTCTTATACCGACACAGTCGTGGTTGTAACATGCAATCCTGTATCAAAATGGAGT 1023
QY 278 PheProProSerAspGlnSerLys-----ValAlaAsp 288
Db 1024 GGGCCACCTAAGGACAAACCAAGTACACTACAGATGAGGCTGTACAGCATGTCCGTGAT 1083
QY 289 LeuValLysGlnHisGlyIleIleTyr---ValLeuGluValAlaLysTyrTyrAspAsp 307
Db 1084 CTCTACAGAGAGAGCATTTGTGAAGTATAGGGTCCAGGACTCTGGTAAGAAAGTCTCCTGAC 1143
QY 308 ProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSerTyrLeu 327
Db 1144 AGCAGTGAGCCAGACATACAGGAGCTT----- 1170
QY 328 ProGlyPheIleSerMetHisAsp---ValAlaTyrPheAspPheLeuAsnArgValHis 346
Db 1171 ---TCATTTACAGAGTTGAGAGACAAACTACTTTCCTTGTATCCTCTCAATGACGTTCAC 1227
QY 347 ValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeuPro----- 361
Db 1228 GTTGCAAAAGTAAATCAAGCTGAGGCAGAGTTTTTGGAAAAAATCAGAAGGATATAGAGTA 1287
QY 362 -----HisProTrpLeuAsn----- 366
Db 1288 GGGTGGAGTGATGAAATTTCTGGGCTTTTGACTGTGGTGGTCAGCAGTGGGTGTCAGAATCT 1347
QY 367 -----LeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380
Db 1348 TGTTCCTCTGTGAAACCTCGCCAAACCTAGCATGAAGACCTTGAATACATAGAGAG 1407
QY 381 ValValLysAspIleLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400
Db 1408 CTGAAAAAA-----CTAATAGAAAAGGAAGCAATACCAGCACCTGCTCCAATA----- 1455
QY 401 ThrAsnArgAsnLysTrpAspAsnArg-----MetSerAlaMetIleProGlu 416
Db 1456 -----GAGCAGCGATGGACAGCTCGAAGTAAGAGCCCCCATTAGTCTCTGCATTCAGCACT 1509
QY 417 IleAspGluAspValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeu 436
Db 1510 TCAGAGGATGATATTTTCTCATGGTTGGTATATCATGTACCTCCGACAGCAGACCCCT 1569
QY 437 ProGluValGluSerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLys 456
Db 1570 CGCCAGAGAAAGGACATCACAGATGAATTTTCCACTAT----- 1608
QY 457 IleLysGlnTyrLeuMetHisTyrThrSerLysGluAspTrp-----Ile 471
Db 1609 -----AGACATTTGACACAGAAACAATTGTGGATCAATTTTCTGCGTAT 1653
QY 472 GluHisPheGlySer----- 476

```
Db 1654 GAACATTGGCGTAAATGAGATACCAAAAGACAAAGAACTTGAAGCCTTACAGGCA 1713
Qy 477 -----LysTrpAspAspPheSerLysArgLysAspLeuPheAspPro 490
Db 1714 AGAATAAGAAAACGTTTCCAGTGGATGCATACAAACAAAGCACGTAGGAGCTGGACCCA 1773
Qy 491 LysLysLeuLeuSer 495
Db 1774 AATAGAATCCTCTCC 1788

RESULT 13
US-09-423-468A-12
; Sequence 12, Application US/09423468A
; Patent No. 6469149
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
; APPLICANT: Mark William Davey
; APPLICANT: Jens Ostergaard
; APPLICANT: Marc Charles Ernest Van Montagu
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLES.001APC
; CURRENT APPLICATION NUMBER: US/09/423,468A
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: NL 1006000
; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Brassica oleracea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)...(1846)
US-09-423-468A-12
```

```
Alignment Scores:
Pred. No.: 3.23e-11 Length: 2034
Score: 175.50 Matches: 106
Percent Similarity: 38.07% Conservative: 95
Best Local Similarity: 20.08% Mismatches: 229
Query Match: 6.76% Indels: 99
DB: 4 Gaps: 20
```

```
US-10-014-101-4 (1-501) x US-09-423-468A-12 (1-2034)
Qy 31 LeuAsnLeuThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGly 50
Db 324 CTCTCCCCGAAGATCTCCACA--CCGTCTCTAACTGAGTGGA----- 365
Qy 51 AsnIleThrThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSer 70
Db 366 ---CTCAGAGGTCAGACAGCACTTTAAACCAG-CCGGAGACTCTCGCCGATCTCGAA 421
Qy 71 ArgLeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGln 90
Db 422 GCTCTCGTCAAGGAAGCTCATGAGAAGAAGAAC-----AGGATCCGACCCGTTGGATCC 475
Qy 91 GlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCys 110
Db 476 GGTCCTTCCCCCAATGGG---ATCGGTTTGTCTCGCTCGGGGATGGTGAATTGGCGCTC 532
Qy 111 IleThrAspValVal---ValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThr 129
Db 533 ATGGACAAGGTCCTCGAGGTGGATAAAGAGAAGAGAGATCCGTGTGCAGGCTGGGATT 592
Qy 130 LeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerProValSerTrpThr 149
Db 593 AGGGTTCAGCAGCTTGTGTGACGCCATTCAAGAGTATGGTCTCACTCTCCAGAACTTTGCT 652
Qy 150 AspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGlnVal 169
```

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Db 653 TCCATTAGAGAGCAGCAGATTGGTGGCATCATTCAGGTTGGGGCACATGGGACAGGTGCT 712
Qy 170 PheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGly 189
Db 713 ---AGATTGCCTCCTATCGATGAGCAAGTGAATGGCATGAAGCTTGTCACTCCTGCTAAG 769
Qy 190 GluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGly 209
Db 770 GGAACTATTGAGCTTTCTAAGGATAAATGATCCGGAGCTCTTTTCATCTTGTGCTGATGGC 829
Qy 210 LeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLysArg 229
Db 830 CTTGGTGGACTTGGAGTTGTT-----GCTGAGGTCAACCTCCAGTGCCTGGAAGACAG 883
Qy 230 AlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArg 249
Db 884 GAGCTTTTGGAGCACACTTACGTCTCCACCTTGGGAAGAGATCAAGAAAAATCACAATAAG 943
Qy 250 LeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGlnIle 266
Db 944 TTGCTCTCTACAAATAAGCATGTCAAGTACCTGCTATATATTCATATACTGACACGGTCGTG 1003
Qy 267 PheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys--- 285
Db 1004 GTTGTACATGCAACCTGTATCAAAATGGAGTGGGGCACCTTAAGGACAAACCAAGTAC 1063
Qy 286 -----ValAlaAspLeuValLysGlnHisGlyIleIleTyr 297
Db 1064 ACTACAGAGGAGGCTTTAAAGCATGTCCGTGACCTGTATAGAGAGCATTTTAAGTAT 1123
Qy 298 ---ValLeuGluValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysVal 316
Db 1124 AGGGTCCAGGACTCTAGTAAGAAGACTCCTGACAGTAGGGAGCCAGACATTAAACGAGCTT 1183
Qy 317 IleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAsp--- 335
Db 1184 -----TCATTTACAGAGTTGACAGATAAG 1207
Qy 336 ValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeu 355
Db 1208 CTGATTGCCCTAGATCCTCTCAATGACGTTTCACGTTGGAAAAAGTGAATCAAGCTGAGGCT 1267
Qy 356 GlyLeuTrp----- 358
Db 1268 GAGTTTGGAAAAAATCAGAAGGATACAGAGTAGGTGGAGTGATGAAATCCTGGGCTTT 1327
Qy 359 -----GluLeuProHisProTrpLeuAsnLeuTyrVal 369
Db 1328 GACTGTGGTGGTCAACAGTGGGTATCAGAAACTTGTTCCTGCTGGAACCTCTCGCTAAA 1387
Qy 370 ProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGln 389
Db 1388 CCTAGCATGAAAGACCTTGAGTACATAGAA---CAGCTGAAAGAGTTGATACAAAAAGAA 1444
Qy 390 LysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsn---ArgAsnLysTrpAspAsn 408
Db 1445 -----GCAATACCAGCACCTTCTCCCATAGAGCAGCGTTGGACAGGC 1486
Qy 409 Arg-----MetSerAlaMetIleProGluIleAspGluAspValIleTyrIle 424
Db 1487 CGAAGTAAGAGCCCTATGAGTCTGTCATTTCAGCACTGACAGAGGAGACATTTTCTCATGG 1546
Qy 425 IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1547 GTTCGTATAATCATGTATCTCCGACAGCAGACCCCTCCGACAGAAAGGACATCAGCGAT 1606
Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db 1607 GAATTTTCCACTATAGACATTTGACACAGGCAAAATGTGGGAC-----CAGTAT 1657
Qy 465 ThrSerLysGluAspTrpIle----- 471
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Db 1658 TCTGCGTATGAACATTGGGCTAAATAATTGAGATACCAAAGGATAAAAGAGAACTTGAAGCC 1717
QY 472 -----GluHisPheGlySerLysTrp-----AspAspPheSerLysArgLysAspLeu 487
Db 1718 CTACAAGAAAGACTCAGAAAACGATTCCCGGTGGATGCATACAACAAAGACACGAAGGGAG 1777
QY 488 PheAspProLysLysLeuLeuSer 495
Db 1778 CTGGACCCCAACACAGAATTCTCTCA 1801

RESULT 14
US-09-630-983A-4
; Sequence 4, Application US/09630983A
; Patent No. 6630330
; GENERAL INFORMATION:
; APPLICANT: Porro, Danilo
; APPLICANT: Sauer, Michael
; TITLE OF INVENTION: Ascorbic Acid Production from Yeast
; FILE REFERENCE: 2028.594000
; CURRENT APPLICATION NUMBER: US/09/630,983A
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: Brassica oleracea
US-09-630-983A-4

Alignment Scores:
Pred. No.: 3,31e-11 Length: 2064
Score: 175.50 Matches: 106
Percent Similarity: 38.07% Conservative: 95
Best Local Similarity: 20.08% Mismatches: 229
Query Match: 6.76% Indels: 99
DB: 4 Gaps: 20

US-10-014-101-4 (1-501) x US-09-630-983A-4 (1-2064)

QY 31 LeuAsnLeuThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGly 50
Db 336 CTCTCCCGAAGATCTCCACA---CCGTCTCTAACTGGAGTGGTA----- 377
QY 51 AsnIleThrThrValThrProGlyGlyValIleCysProSerThrAlaAspIleSer 70
Db 378 ---CTCACGAGGCCAGACCAGGAACCTTAACACAG-CCGGAGACTCTGCCGATCTCGAA 433
QY 71 ArgLeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGln 90
Db 434 GCTCTCGTCAAGGAAGCTCATGAGAAGAGAAC-----AGGATCCGACCCGTTGGATCC 487
QY 91 GlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCys 110
Db 488 GGTCTTTCCCCCAATGGG---ATCGGTTTGTCTCGCTCGGGGATGGTGAATTTGGCGCTC 544
QY 111 IleThrAspValVal---ValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThr 129
Db 545 ATGGACAAGGTCTCGAGGTGGATAAAGAGAAGAGAGAGTCCGCTGTGCAGGCTGGGATT 604
QY 130 LeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerProValSerTrpThr 149
Db 605 AGGGTTCAGCAGCTTGTTCAGCGCCATTCAAGAGTATGGTCTCACTCTCCAGAACTTTTGCT 664
QY 150 AspTyrLeuHisIleThrValGlyThrLeuSerAsnGlyGlyIleGlyGlyGlnVal 169
Db 665 TCCATTAGAGACGACAGATTGGTGGCATCATTCAGGTTGGGGCACATGGGACAGGTGCT 724
QY 170 PheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGly 189
Db 725 ---AGATTGCCTTCATCGATGAGCAAGTGAAGTGGCATGAAGCTTGTCACTCTCTAAG 781
QY 190 GluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGly 209

Db 782 GGAACATTATTGAGCTTTCTAAGGATAATGATCCGGAGCTCTTTTCATCTTGTCTGATGTGGC 841
QY 210 LeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLysArg 229
Db 842 CTTGGTGGACTTGGAGTTGTT-----GCTGAGGTACCCCTCCAGTCGCTTGAAGACAG 895
QY 230 AlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArg 249
Db 896 GAGCTTTTGGAGCACACTTACGTCTCCACCTTGGAAAGAGATCAAGAAAAATCACAAAAAG 955
QY 250 LeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGlnIle 266
Db 956 TTGCTCTCTACAAATAAGCATGTCAAGTACCTGTATATTCATATATACTGACACGGTCGTG 1015
QY 267 PheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys--- 285
Db 1016 GTTGTTCATGCAACCCCTGTATCAAAATGGAGTGGGCACCTAAGGACAAACCAAAGTAC 1075
QY 286 -----ValAlaAspLeuValLysGlnHisGlyIleIleTyr 297
Db 1076 ACTACAGAGGAGGCTTTAAAGCATGTCCGTGACCTGTATAGAGAGACGATTTTAAGTAT 1135
QY 298 ---ValLeuGluValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysVal 316
Db 1136 AGGGTCCAGGACTCTAGTAAGAAGACTCTCAGACGTAGGGAGCCAGACATTAAACGAGCTT 1195
QY 317 IleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAsp--- 335
Db 1196 -----TCATTTACAGAGTTGAGAGATAAG 1219
QY 336 ValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeu 355
Db 1220 CTGATTGCCCTAGATCCTCTCAATGACGTTACGTTGGAAAAGTGAATCAAGCTGAGGCT 1279
QY 356 GlyLeuTrp----- 358
Db 1280 GAGTTTGGAAAAAATCAGAAGGATACAGAGTAGGGTGGAGTGATGTAATCCTGGGCTTT 1339
QY 359 -----GluLeuProHisProTyrLeuAsnLeuTyrVal 369
Db 1340 GACTGTGGTGGTCAACAGTGGGTATCAGAAACTTGTTCCTGCTGGAACCTCTCGCTAAA 1399
QY 370 ProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGln 389
Db 1400 CCTAGCATGAAGACCTTGAGTACATAGAA---CAGCTGAAAGAGTTGATACAAAAAGAA 1456
QY 390 LysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsn---ArgAsnLysTrpAspAsn 408
Db 1457 -----GCAATACCAAGCACTTCTCCCATAGAGCAGCGTTGGACAGGC 1498
QY 409 Arg-----MetSerAlaMetIleProGluIleAspGluAspValIleTyrIle 424
Db 1499 CGAAGTAAGAGCCCTATGAGTCTCTGCATTGACGACTGCAGAGGAGGACATTTTCTCATGG 1558
QY 425 IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1559 GTTGGTATAATCATGTATCTCCGACAGCAGACCCCTCGCCAGAGAAAGACATCACCGAT 1618
QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db 1619 GAATTTTCCACTATAGACATTTGACACAGGCAAAATTTGTGGGAC-----CAGTAT 1669
QY 465 ThrSerLysGluAspTrpIle----- 471
Db 1670 TCTCGGTATGAACATTGGGCTAAATTTGAGATACCAAGGATAAAGAGAACTTGAAGCC 1729
QY 472 -----GluHisPheGlySerLysTrp-----AspAspPheSerLysArgLysAspLeu 487
Db 1730 CTACAAGAAAGACTCAGAAAAACGATTTCCCGTGGATGCATACACAAAGACGACGAAGGAG 1789
QY 488 PheAspProLysLysLeuLeuSer 495
Db 1790 CTGGACCCCAACACAGAATTCTCTCA 1813

RESULT 15
US-09-328-352-1897
; Sequence 1897, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1897
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1897

Alignment Scores:
Pred. No.: 2.6e-11 Length: 1407
Score: 174.00 Matches: 104
Percent Similarity: 34.22% Conservative: 77
Best Local Similarity: 19.66% Mismatches: 196
Query Match: 6.70% Indels: 152
DB: 4 Gaps: 20

US-10-014-101-4 (1-501) x US-09-328-352-1897 (1-1407)

QY	35	LeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThr	54
Db	67	ATTAAACCGATGCTGATAGTCGCAAACTGGGTAAAGATCATACCAAGCATTTAAT	126
QY	55	ValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGln	74
Db	127	CCGAACCATCGGTATCGTTTTCATCAACGACTGAACAAGTTCAGGAAGTTGTGAAG	186
QY	75	TyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeu	94
Db	187	CTTGCA-----AACAGTTTAATATCGCAATTACACCGTCAGGT-----	225
QY	95	AsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIleThrAspVal	114
Db	226	---GGACGTACAGGACTTCTGCTGGTGTGTAGCAACCAAT-----GGTGAATTT	273
QY	115	ValValSerLysAspLys-----LysTyrAla	123
Db	274	GTCATTAGCATGGACAAATGAACACAGATTCTTGAGTTCTCCGGCAGACCGTATGGTT	333
QY	124	AspValAlaAlaGlyThrLeuTrpValAspValLeuLysThrAlaGluLysGlyVal	143
Db	334	CGTGACAACTGGTGTGTGACTGAGCAATTGCAAAATATGCAGAAAGACGGTATG	393
QY	144	---SerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsn	162
Db	394	TATTATCCGTTGACTTTGGCTCAGCGGGTTCTAGTCAGATTGGCGTAAATATCGGTACC	453
QY	163	GlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeu	182
Db	454	AACGCTGGTGGTATTAAAGTCATTAAATATGGCATGACCGCTAACTGGGTACTCGGTTTA	513
QY	183	AspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeu-----	198
Db	514	ACTGTAGTACCGGGTAAGGGCGACATTTTACGTTTAAACAAAGGCATGATTAATAATGCA	573
QY	199	---AsnProGluLeuPheTyrGlyValLeuGlyGlyLeuGlnPheGlyIleIleThr	217
Db	574	ACTGGTTATGCATTACAGCATTGTGTTTATGGTGGTGAAGGTACATTAGGTTTAGTGACT	633
QY	218	ArgAlaArgIleValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyr	237
Db	634	GAAGCAGAAATTAACCTTGAGCGTCAACCAACAAAC-----CTACAAGTTTAGTT	684

Search completed: April 7, 2004, 11:48:47
Job time : 4274 secs

QY	238	SerAspPheThrThrPheThrLysAspGlnGluArgIleLeuSerMetAlaAsnAspIle	257
Db	685	TTAGGTGTTCTGATTTTGTGCAGTAATGCCTGTGTATCATGCTTTCCAAAAAGATATC	744
QY	258	GlyValAspTyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhe	277
Db	745	GACTTAACCTGCATTGAG-----TTC	765
QY	278	PheProProSerAspGlnSerLysValAlaAsp-----LeuVal	290
Db	766	TTTGGTGAGCTTGCAATGCCAAAAGTACTCGACCGTGGTCATGTTCAACGTCCTTGA	825
QY	291	LysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyrAspAspProhenLeu	310
Db	826	ACTCAATGTCCATTCTATGTATGCTTGAG-----TTTGAAGCGCCATACGAA	873
QY	311	ProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer-----TyrLeu	327
Db	874	CCGATTATCGACAAAGCAATGGAGATTTTCGAGCACCTGTATGGAACAAGTTGGGTACTT	933
QY	328	ProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgValHisVal	347
Db	934	GATGGTCTAATGAGCCAGAGC-----CTTGACCAAGTAGAG---969	
QY	348	GluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeu	367
Db	970	-----AGCTTGTGGCGT-----981	
QY	368	TyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeu	387
Db	982	-----TTA	984
QY	388	LysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAsp	407
Db	985	CGCAAGATATTTCTGAATCAATCGCGCGCTTTATTCCA-----TACAAA	1029
QY	408	AsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIleGlyLeu	427
Db	1030	AACGATATTTTCAATTAATTAATCTACGTACCTGTCATTATTCGTGAAATTGATGCGATT	1089
QY	428	LeuGlnSerAlaThrPro-----433	
Db	1090	GTTCAAGAAAACTATCCTGACTTTGAAATTTGCTGGTTCGGCCATATCGGCGACGGTAAAC	1149
QY	434	-----LysAsp-----LeuProGluVal	439
Db	1150	TTGCACCTTAAATATTTTAAACCTGAAAACTTAACCAAGGATGAGTTCTTTGCGAAATGT	1209
QY	440	GluSerValAsnGluLysIleIleArgPheCysLys-----451	
Db	1210	CAGGTGGTGAATAAATATGTGTTTGATACCGTTAAAAAATACGATGGCTCAATCTCTGCC	1269
QY	452	-----AspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSerLysGluAsp	469
Db	1270	GAGCATGGCGTAGGTATGACGAAAAAGCCATATTTGGAAATATTCGGCTCAGCTGAAGAA	1329
QY	470	TrpIleGluHisPheGlySerLysTrpAspPheSerLysArgLysAspLeuPheAsp	489
Db	1330	---ATCGAATAT-----ATGAAAGCTTTGAAAAAAGTATTTTGAC	1365
QY	490	ProLysLysLeuLeuSerProGlyGln	498
Db	1366	CCGAAAGGTATTATGAATCCAGGTAAA	1392

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 05:49:35 ; Search time 629 Seconds
(without alignments)
3383.700 Million cell updates/sec

Title: US-10-014-101-4
Perfect score: 2596
Sequence: 1 MANLRMLITLITVLMITKSS.....SKRKDLFDPKLLSPGQDIF 501

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO spool/US10014101/runat_05042004_154153_8568/app query.fasta_1.647
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10014101@cgn_1_1_470@runat_05042004_154153_8568 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2596	100.0	1506	6	ABK28625
2	2596	100.0	1506	8	ACC85294
3	2579	99.3	1548	3	AAC43214
4	2226.5	85.8	2991	6	ABK28607
5	2226.5	85.8	2991	8	ACC85276
6	1822	70.2	1575	3	AAC42983
7	1822	70.2	1575	6	ABZ14284
8	1822	70.2	1575	6	ABK28627

9	1822	70.2	1575	7	ADA68648	ADA68648	Arabidops
10	1822	70.2	1575	8	ACC85296	ACC85296	Arabidops
11	1539.5	59.3	2782	6	ABK28609	ABK28609	DNA encod
12	1539.5	59.3	2782	8	ACC85278	ACC85278	Arabidops
13	1292	49.8	1572	6	ABK28626	ABK28626	cdNA enco
14	1292	49.8	1572	8	ACC85295	ACC85295	Arabidops
15	1184	45.6	1611	6	ABK28628	ABK28628	cdNA enco
16	1184	45.6	1611	8	ACC85297	ACC85297	Arabidops
17	1184	45.6	1620	6	ABK28632	ABK28632	cdNA enco
18	1184	45.6	1620	8	ACC85301	ACC85301	Arabidops
19	1141.5	44.0	1608	3	AAC86501	AAC86501	DNA encod
20	1141	44.0	1605	2	AAK02914	AAK02914	Z. mays c
21	1091	42.0	1566	7	ADA71115	ADA71115	Rice gene
22	1091	42.0	1593	7	ADA69430	ADA69430	Rice gene
23	1076	41.4	1677	7	ADA70177	ADA70177	Rice gene
24	1074	41.4	1587	7	ADA69574	ADA69574	Rice gene
25	1063.5	41.0	1590	7	ADA69773	ADA69773	Rice gene
26	1056.5	40.7	1728	6	ABK28624	ABK28624	cdNA enco
27	1056.5	40.7	1728	8	ACC85293	ACC85293	Arabidops
28	1014	39.1	6733	2	AAK02913	AAK02913	Z. mays c
29	993	38.3	1515	6	ABK28629	ABK28629	cdNA enco
30	993	38.3	1515	8	ACC85298	ACC85298	Arabidops
31	920.5	35.5	1936	6	ABK28611	ABK28611	DNA encod
32	920.5	35.5	1936	8	ACC85280	ACC85280	Arabidops
33	920.5	35.5	2805	6	ABK28610	ABK28610	DNA encod
34	920.5	35.5	2805	8	ACC85279	ACC85279	Arabidops
35	920.5	35.5	2814	6	ABK28631	ABK28631	DNA encod
36	920.5	35.5	2814	8	ACC85300	ACC85300	Arabidops
37	905.5	34.9	3302	6	ABK28608	ABK28608	DNA encod
38	905.5	34.9	3302	8	ACC85277	ACC85277	Arabidops
39	903.5	34.8	2236	6	ABK28606	ABK28606	DNA encod
40	903.5	34.8	2236	8	ACC85275	ACC85275	Arabidops
41	835	32.2	1602	2	AAK02919	AAK02919	Z. mays c
42	791	30.5	503	3	AAC36788	AAC36788	Arabidops
43	457	17.6	1464	7	ABT32136	ABT32136	Benzodiaz
44	457	17.6	32539	7	ABT32129	ABT32129	Benzodiaz
45	226.5	8.7	1545	5	AAH65600	AAH65600	C glutami

ALIGNMENTS

RESULT 1

ABK28625
ID ABK28625 standard; cdNA; 1506 BP.

XX AC ABK28625;

XX DT 09-APR-2002 (first entry)

XX DE cdNA encoding A. thaliana cytokinin oxidase AtCKX2.

XX KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarpy; gene; ss.

XX OS Arabidopsis thaliana.

XX PN WO200196580-A2.

XX PD 20-DEC-2001.

XX PF 18-JUN-2001; 2001WO-EP006833.

XX PR 16-JUN-2000; 2000EP-00870132.

XX PR 27-DEC-2000; 2000US-0258415P.

XX PR 16-MAR-2001; 2001EP-00870053.

XX PA (SCHM/) SCHMULLING T.

XX PA (WERN/) WERNER T.

XX PI Schmulling T, Werner T;

XX DR WPI; 2002-130736/17.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 146-147; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,19e-265 Length: 1506
Score: 2596.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-014-101-4 (1-501) x ABK28625 (1-1506)

QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20
DB 1 ATGGCTAATCTTCGTTTAATGATCACTTTAATCAGCGTTTAAATGATCACCAATCATCA 60
QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProser 40
DB 61 AACGGTATTAAATGATTTACCTAATCCCTTAACCTCACCCCTCTCTACCGATCCTTTC 120
QY 41 IleIleSerAlaIleSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
DB 121 ATCATCTCCGAGCCTCTCATGACTTCGGAAACATAACACCGTGACCCCGCGCGGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80
DB 181 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCTCTCAATACGCGCAACGGA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
DB 241 AGTACATTCCAAGTAGCGGCTCGTGGCCAAAGGCACTCCTTAAACGCGCAAGCCTCGGTC 300
QY 101 SerGlyGlyValIleValAlaAsnMetThrCysIleThrAspValValValSerLysAspLys 120
DB 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAAGACAAG 360
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysThrAlaGlu 140
DB 361 AAGTACGCTGACGTGGCGGCGGACGTTATGGTGGATGTGCTTAAAGACGCGGAG 420
QY 141 LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyThrLeu 160
DB 421 AAAGGGGTGTCGCGGTTCTTGGACGGATTATTGTCATATAACCGTCGAGGAACGTTG 480
QY 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180

DB 481 TCGAATCGTGGAATTGGTGGTCACTGTTTCGAAAACGGTCTCTTGTAGTAACGTCCTT 540
QY 181 GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200
DB 541 GAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCA 600
QY 201 GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg 220
DB 601 GAATTGTTCTATGGAGTGTAGGAGGTTGGGTCAATTTGGAATTATAACGAGAGCCAGA 660
QY 221 IleValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPhe 240
DB 661 ATTGTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTC 720
QY 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260
DB 721 ACAACTTTTACAAAGGACCAAGACGTTTGATATCAATGGCAACGATATTGGAGTCGAC 780
QY 261 TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProPro 280
DB 781 TATTTAGAAAGGTCAAAATATTCTATCAAAACGGTGTGCTGTGACACCTCTTTTCCCACCT 840
QY 281 SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu 300
DB 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGA 900
QY 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320
DB 901 GTAGCCCAAGTATTATGATGATGCCAATCTCCCATCATCAGCAAGTTATTGACACATTA 960
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340
DB 961 ACGAAAACATTAAAGTTACTTGCCTGGGTTTCATATCAATGCCACGCTGGCCTACTTCGAT 1020
QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeu 360
DB 1021 TTCTTGAACCGTGATCATGTGGAAGAAATAAACTCAGATCTTTGGGATTATGGGAACCT 1080
QY 361 ProHisProTrpLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380
DB 1081 CCTCATCTTGGCTTAAACCTCTACGTTCCCTAAATCTCGGATTCGATTTTCATAACGGT 1140
QY 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400
DB 1141 GTTGTCAAAGACATCTTCTTAAAGCAAAATCAGCTTCGGGACTCGCTCTCTCTATCCA 1200
QY 401 ThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp 420
DB 1201 ACAACCCGGAATAAATGGGACAATCGTATGTCGGCGATGATACCAGAGATCGATGAAGAT 1260
QY 421 ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu 440
DB 1261 GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAG 1320
QY 441 SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr 460
DB 1321 AGCGTTAACGAGAAGATAATTAGGTTTTCGAAGGATTGAGCATTTTGGATCAAATGAATAT 1380
QY 461 LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp 480
DB 1381 CTAATGCATTATATAGTAAGAAGATTGGATTGAGCATTTTGGATCAAATGAATGATGAT 1440
QY 481 PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle 500
DB 1441 TTTTCGAAGAGGAAGATCTATTTGATCCCAAGAACTGTTTATCTCCAGGCAAGACATC 1500
QY 501 Phe 501
DB 1501 TTT 1503

RESULT 2

ACC85294

ID ACC85294 standard; cDNA; 1506 BP.

XX AC ACC85294;
XX 18-SEP-2003 (first entry)
XX Arabidopsis cytokinin oxidase-like protein 2 cDNA.
XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX Arabidopsis thaliana.
OS WO2003050287-A2.
XX 19-JUN-2003.
XX 10-DEC-2002; 2002WO-EP013990.
XX 10-DEC-2001; 2001US-00014101.
XX (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX Schmullling T, Werner T;
PI WPI; 2003-541577/51.
XX Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX Claim 3; Page 167-168; 177pp; English.
XX The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.19e-265 Length: 1506
Score: 2596.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-014-101-4 (1-501) x ACC85294 (1-1506)
QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20
Db 1 ATGGCTAATCTTCGTTTAAATGATCACTTTAATCACGGTTTAAATGATCACCAATCATCA 60
QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40
Db 61 AACGGTATTAAATTGATTTTACCTAAATCCCTTAACTCACCTCTCTACCGATCCTTCC 120
QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
Db 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACATACACACCGTGACCCCCGCGCGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80

Db 181 ATCTGCCCTCTCCACCGCTGATATCTCTCGTCTCTCCATACGCGCAACGGA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
Db 241 AGTACATTCCAAGTAGCGGCTCGTGGCCCAAGCCACTCTCTTAAACGCGCAAGCCTCGGTC 300
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys 120
Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAAGACAAG 360
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGlu 140
Db 361 AAGTACGCTGACGTGGCGCGGACGTTATGGGTGGATGTGCTTAAAGAACGCGGAG 420
QY 141 LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160
Db 421 AAAGGGGTGTCCGCCGTTTCTTGGACGGATTATTGTCATATAACCGTCGGAGAACGTTG 480
QY 161 SerAsnGlyGlyIleGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180
Db 481 TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCTCTCTTGTAGTAACGTCCTT 540
QY 181 GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200
Db 541 GAATTGGACGTTATTACTGGGAAAGGTGAATGTGACATGCTCGCGACAGCTAAACCCA 600
QY 201 GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg 220
Db 601 GAATTGTTCTATGGAGTCTTAGGAGGTTTGGGTCAATTTGGAATTATATAACGAGAGCCAGA 660
QY 221 IleValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPhe 240
Db 661 ATTGTTTTGGACCATGCACCTAAACCGGGCCAAATGGTTTCGGATGCTCTACAGTATTTC 720
QY 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260
Db 721 ACAACTTTTACAAAGGACCAAGAACGTTTGTATATCAATGGCAACGATATTGGAGTCGAC 780
QY 261 TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProPro 280
Db 781 TATTTAGAAGGTCAATATTTCTATCAACCGGTGCGTTGACACCTCTTTTTTCCACCT 840
QY 281 SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu 300
Db 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGCGTATCATCTATGTCTTGAA 900
QY 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320
Db 901 GTAGCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA 960
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340
Db 961 ACGAAAACATTAAAGTTACTTGGCCGGGTTTCATATCATATGACGACGCGTGGCCTACTCGAT 1020
QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu 360
Db 1021 TTCTTGAACCGTGATACATGTCGAAGAAAAATAAACTCAGATCTTTGGGATTATGGGA 1080
QY 361 ProHisProTrpLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380
Db 1081 CCTCATCCTTGGCTTAACCTTACGTTCTCTAAATCTCGGATTCTCGATTTTTCATAACGGT 1140
QY 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400
Db 1141 GTTGTCAAAGACATTCTTCTTAAGCAAAATCAGCTTCGGACTCGCTCTTCTCTATCCA 1200
QY 401 ThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp 420
Db 1201 ACAAACCGGAATAAATGGGACAAATCGTATGTGCGCGATGATACAGAGATCGATGAAGAT 1260
QY 421 ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu 440

Db	1261	GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAG	1320	PR	27-MAY-1999;	99US-0136392P.
				PR	28-MAY-1999;	99US-0136782P.
QY	441	SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr	460	PR	01-JUN-1999;	99US-0137222P.
				PR	03-JUN-1999;	99US-0137528P.
Db	1321	AGCGTTAACGAGAGAGATAAATAGGTTTTCGAAGGATTCAGGTATTAAAGCAATAT	1380	PR	04-JUN-1999;	99US-0137502P.
				PR	07-JUN-1999;	99US-0137724P.
QY	461	LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp	480	PR	08-JUN-1999;	99US-0138094P.
				PR	10-JUN-1999;	99US-0138540P.
Db	1381	CTAATGCATTATACTAGTAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT	1440	PR	10-JUN-1999;	99US-0138847P.
				PR	14-JUN-1999;	99US-0139119P.
QY	481	PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle	500	PR	16-JUN-1999;	99US-0139452P.
				PR	16-JUN-1999;	99US-0139453P.
Db	1441	TTTTCGAAGAGAAAGATCTATTGTATCCCAAGAAACTGTTATCTCCAGGCAAGACATC	1500	PR	17-JUN-1999;	99US-0139492P.
				PR	18-JUN-1999;	99US-0139454P.
QY	501	Phe 501		PR	18-JUN-1999;	99US-0139455P.
				PR	18-JUN-1999;	99US-0139456P.
Db	1501	TTT 1503		PR	18-JUN-1999;	99US-0139457P.
				PR	18-JUN-1999;	99US-0139458P.
RESULT 3						
AAC43214						
ID	AAC43214 standard; DNA; 1548 BP.					
XX						
AC	AAC43214;					
XX						
DT	17-OCT-2000 (first entry)					
XX						
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 38443.					
XX						
KW	Hybridisation assay; genetic mapping; gene expression control;					
KW	protein identification; signal transduction pathway; metabolic pathway;					
KW	promoter; termination sequence; ss.					
XX						
OS	Arabidopsis thaliana.					
XX						
PN	EP1033405-A2.					
XX						
PD	06-SEP-2000.					
XX						
PF	25-FEB-2000; 2000EP-00301439.					
XX						
PR	25-FEB-1999;	99US-0121825P.				
PR	05-MAR-1999;	99US-0123180P.				
PR	09-MAR-1999;	99US-0123548P.				
PR	23-MAR-1999;	99US-0125788P.				
PR	25-MAR-1999;	99US-0126264P.				
PR	29-MAR-1999;	99US-0126785P.				
PR	01-APR-1999;	99US-0127462P.				
PR	06-APR-1999;	99US-0128234P.				
PR	08-APR-1999;	99US-0128714P.				
PR	16-APR-1999;	99US-0129845P.				
PR	19-APR-1999;	99US-0130077P.				
PR	21-APR-1999;	99US-0130449P.				
PR	23-APR-1999;	99US-0130510P.				
PR	28-APR-1999;	99US-0130891P.				
PR	30-APR-1999;	99US-0131449P.				
PR	04-MAY-1999;	99US-0132048P.				
PR	05-MAY-1999;	99US-0132484P.				
PR	06-MAY-1999;	99US-0132485P.				
PR	06-MAY-1999;	99US-0132486P.				
PR	06-MAY-1999;	99US-0132487P.				
PR	07-MAY-1999;	99US-0132863P.				
PR	11-MAY-1999;	99US-0134256P.				
PR	14-MAY-1999;	99US-0134218P.				
PR	14-MAY-1999;	99US-0134219P.				
PR	14-MAY-1999;	99US-0134221P.				
PR	14-MAY-1999;	99US-0134370P.				
PR	18-MAY-1999;	99US-0134768P.				
PR	19-MAY-1999;	99US-0134941P.				
PR	20-MAY-1999;	99US-0135124P.				
PR	21-MAY-1999;	99US-0135353P.				
PR	24-MAY-1999;	99US-0135629P.				
PR	25-MAY-1999;	99US-0136021P.				

Db 901 GTAGCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGTTATTGACACATTA 960
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340
Db 961 ACGAAAACATTAAGTTACTTGGCCGGTTTCATAATCAATGACGACGTGGCCTACTTCGAT 1020
QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu 360
Db 1021 TTCTGTGAACCGTGTACATGTGCAAGAAATAAACTCAGATCTTTGGGATTATGGGAAC 1080
QY 361 ProHisProTyrLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380
Db 1081 CCTCATCCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATCTCGATTTTCATAACGGT 1140
QY 381 ValValLysAspIleLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400
Db 1141 GTTGTCAAAGACATTTCTTTAAGCAAAATCAGCTTCGGACTCGCTCTCTCTATCCA 1200
QY 401 ThrAsnArgAsn-----LysTyr 406
Db 1201 ACAACCGGAATAAGTACATATCTTCTTCTTATTTATCTTCAAGAACCAAAATGG 1260
QY 407 AspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIleGly 426
Db 1261 GACATCGTATGTCGGCGATGATACCAGAGATCGATGAGATGTTATATATATATATCGGA 1320
QY 427 LeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluLysIle 446
Db 1321 CTACTACAAATCCGCTACCCCAAGGATCTTCCAGAAGTCGAGAGCGTTAACGAGAAGATA 1380
QY 447 IleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSer 466
Db 1381 ATTAGGTTTGCAGGATTCAGGTATTAGATTAAGCAATATCTAATGCATTATACTAGT 1440
QY 467 LysGluAspTyrIleGluHisPheGlySerLysTyrAspAspPheSerLysArgLysAsp 486
Db 1441 AAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGAAAGAT 1500
QY 487 LeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1501 CTATTTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCTTT 1545
RESULT 4
ABK28607
ID ABK28607 standard; DNA; 2991 BP.
XX AC ABK28607;
XX DT 09-APR-2002 (first entry)
XX DE DNA encoding A. thaliana cytokinin oxidase AtCKX2.
XX KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
XX KW root growth; lateral root; adventitious root; root geotropism; herbicide;
XX KW root meristem; shoot meristem; leaf senescence; parthenocarpy; gene; ds.
XX OS Arabidopsis thaliana.
XX PN WC200196580-A2.
XX PD 20-DEC-2001.
XX PF 18-JUN-2001; 2001WO-EP006833.
XX PR 16-JUN-2000; 2000EP-00870132.
XX PR 27-DEC-2000; 2000US-0258415P.
XX PR 16-MAR-2001; 2001EP-00870053.
XX PA (SCHM/) SCHMULLING T.
XX PA (WERN/) WERNER T.
XX PI Schmullling T, Werner T;

XX WPI; 2002-130736/17.
DR P-PSDB; AAU81968.
XX Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX Claim 3; Page 128-129; 154pp; English.
PS The invention relates to an isolated polynucleotide (I) encoding a novel
XX plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield, and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarpy; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX Sequence 2991 BP; 920 A; 522 C; 521 G; 1028 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 1.06e-225 Length: 2991
Score: 2226.50 Matches: 499
Percent Similarity: 50.00% Conservative: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 85.77% Indels: 499
DB: 6 Gaps: 4
US-10-014-101-4 (1-501) x ABK28607 (1-2991)
QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20
Db 1 ATGGCTAATCTTCGTTTAAATGATCACTTTAATCACGGTTTAAATGATCACCAATCATCA 60
QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40
Db 61 AACGGTATTAAATTTGATTTACCTAAATCCCTTAACCTCACCTCTCTACCGATCTTCC 120
QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
Db 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACATAACCAACCGTGACCCCGCGCGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80
Db 181 ATCTGCCCTCTCTCCACCGCTGATATCTCTCGTCTCTCCATAACGCCGCAACGGA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
Db 241 AGTACATTCCAAGTAGCGGCTCGTGGCCAAGGCCACTCTCTTAACGGCCAAGCCTCGGTC 300
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValSerLysAspLys 120
Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCATCTGACGTGTGTGTTTCAAAAGACAAG 360
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeuLysThrAlaGlu 140
Db 361 AAGTACGCTGACGTGGCGGCGGACGTTATGGTGTGATGTGTTAAGAAGACGCGGAG 420
QY 141 LysGlyValSerProValSerTyrThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160
Db 421 AAAGGGGTGTCGCGGTTTCTTGGACGGATTATTTGCATATATACCGTCGGAGGAACGTTG 480

161 SerAsnGlyGlyIleGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180
 481 TCGAATGGTGAATGGTGGTCAAGTGTTCGAAACGGTCCCTCTTGTAGTAACGTCCTT 540
 181 GluLeuAspValIleThr----- 186
 541 GAATTGGACGTTATTACTGGTACGCACTCTCTAAACCTTTGATGTACATACAACAACAAA 600
 186 ----- 186
 601 ACTGTTTTTTTATAGTATTTTTTCATTTTTTGTACCATAGGTTTTTATAGTT 660
 186 ----- 186
 661 GTGCTAAACTTCTTGCACCACACGTAAGTCTTCGAAACACAAAATGCGTAACGCATCTAT 720
 186 ----- 186
 721 ATGTTTTTTGTACATATTGAATGTTGTTTCATGAGAAATAAAGTAATTACATATACACACA 780
 186 ----- 186
 781 TTTATTGTCGTACATATATAATAATAATTAAAGACAAATTTTTCACAAATGGTAGCGTTAA 840
 186 ----- 186
 841 TTTGGGATTTTGTAAATGTACATGCAATGACGATGCAATGGAGCTTTTCGGTTTTCTTA 900
 186 ----- 186
 901 GATTGTGTAGTATTTCAAATATATATCATTTATTTCTTTCGAATAAAGAGGTGGTATATT 960
 186 ----- 186
 961 TTTAAATAAGCAACATTTTCAGAAATTTTCTTGAATTTTACACTTTTAAATGTTATTGT 1020
 187 ----- GlyLysGlyGluMetLeuThrCysSerArgG1 197
 1021 TAATATGGATTTTGAATAAATAAATTTTCAGGAAAGGTGAAATGTTGACATGCTCGCGACA 1080
 197 nLeuAsnProGluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleTh 217
 1081 GCTAAACCCAGAAATTCCTATGAGTGTAGGAGGTTTGGGTCAATTTGGAATTATAAC 1140
 217 rArgAlaArgIleValLeuAspHisAlaProLys----- 228
 1141 GAGAGCCAGAATTGTTTGGACCATGCACCTAAACGGGTACGTATCATCATATTTTACCA 1200
 228 ----- 228
 1201 TTTGTTTTTAGTCAGCAATTCATTTTTTCATTAGTAATCCGTTTCAATTTCTAAATTTTTT 1260
 228 ----- 228
 1261 AGTCAATAGAAAATGATTCTTATGTCAGAGCTTGATTATTATTAGTGATTTTATTGAGATA 1320
 228 ----- 228
 1321 AAATAAAATATAACCTAAACGGAAATAAATTATTTTACTAATCGGATAATGCTGTATTAAAA 1380
 228 ----- 228
 1381 CATTTTATGATATTACACTAAGAGAGTTAGAGACGTATGGATCACAATAACATGAAGCTTT 1440
 228 ----- 228
 1441 CTTAGATGGTATCCTAAACTAAAGTTAGGTACAAGTTTGGAAATTTAGGTCAAATGCTTA 1500
 228 ----- 228
 1501 AGTTGCATTAAATTTGAACAAAATCTATGCATTGAATAAAAAAAGATATGGATTATTTTA 1560

228 ----- 228
 1561 TAAAGTATAGTCCTTGTAAATCCTAGGACTTGTGTCTAATCTTGTCTTATGCGTGCAAAAT 1620
 228 ----- 228
 1621 CTTTTTGTATGTCAATATATAAATCCTTGTTTATTAGAGTCAAGCTCTTTTCATTAGTCAACT 1680
 228 ----- 228
 1681 ACTCAAAATATACTCCAAAGTTTAGAATATAGTCTTCTGACTAATTAGAAATCTTACAACCG 1740
 228 ----- 228
 1741 ATAAACGTTTACAATTTGGTTATCATTTTAAAAAACAGATTGGTCAATAATATACGATGAC 1800
 228 ----- 228
 1801 GTTCTGTTTTTAGTTTCATCTATTCACAAAATTTTATATAAATTATTTTCAAGAAAAATATTGA 1860
 228 ----- 228
 1861 AATACTATCTGTAATATGTTTCTTTATATATGTGTGTATATAAATTTAAATGGGATTGTTT 1920
 229 ----- ArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrTh 242
 1921 TCTCTAAATGAAATTTGTGTAGGCC-AAATGGTTTCGGATGCTCTACAGTGATTTCAACAAC 1979
 242 rPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLe 262
 1980 TTTTACAAAGGACCACGAACGTTTGTATATCAATGCAACGATATTTGGAGTCGACTATTT 2039
 262 uGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAs 282
 2040 AGAAGGTCAAATATTTCTATCAAACGGTGTCTGACACCTCTTTTTCACCTTTCAGAC 2099
 282 pGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValIleuGluValAl 302
 2100 TCAATCTAAAGTCGTCGATCTAGTCAAGCAACACGATCATCTATGTTCTTGAAGTAGC 2159
 302 aLysTyrTyrAspAspProAsnLeuProIleIleSerLys----- 315
 2160 CAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTACTACACATTATCATTTT 2219
 315 ----- 315
 2220 CATCATCGTTTTTATCATACCATAAAGATATTTTAAATGATTTCATCATTCGCCACCATTAAG 2279
 315 ----- 315
 2280 ATATTTCATCATCATCGTTACATTTTTTTTTTGTGATCTTATGCTTCTCATAAATCTACTA 2339
 316 -----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerM 333
 2340 TTGTGTAGGTTATTGACACATTAACGAAAAACATTAAAGTTACTTGCCTGGGTTTCATATCAA 2399
 333 eHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuA 353
 2400 TGCACGACGTGGCCTACTTCGATTTCTTGAACCGTGTACATGTGGAAGAAAAATAAACTCA 2459
 353 rgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSerA 373
 2460 GATCTTTGGGATTATGGAACTTCTCATCTTGGCTTAACTTAACTTCTACGTTCTCTAAATCTC 2519
 373 rgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAlaAS 393
 2520 GGATTTCTCGATTTTCATAACGGTGTGTGCAAGACATTTCTTCTTAAGCAAAAAATCAGCTT 2579
 393 erGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405
 2580 CGGACTCGCTCTTCTCTATCCAAACAAACCGGAATAA-GTACATACTTCTCTTCATTTCAT 2638
 405 ----- 405

Db 2639 ATTTATCTTCAAGAACCAAGTAAATAAATTTCTATGAACGTGATTATGCTGTATTGTTA 2698
QY 406 --TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleI 425
Db 2699 GATGGACAATCGTATGTCGGCGATGATACCAGAGATCGATGAAGATGTTATATATTA 2758
QY 425 leGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluL 445
Db 2759 TCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAGAGCGTTAACGAGA 2818
QY 445 ysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrT 465
Db 2819 AGATAATTAGTTTTTGAAGGATTCAGGTATTAAGATTAAAGCAATATCTAATGCATTATA 2878
QY 465 hrSerLysGluAspTyrIleGluHisPheGlySerLysTrpAspAspPheSerLysArgL 485
Db 2879 CTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTTCGAAGAGGA 2938
QY 485 ysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 2939 AAGATCTATTGATCCCAAGAAACTGTTATCTCCAGGCAAGACATCTTT 2988

RESULT 5
ACC85276
ID ACC85276 standard; DNA; 2991 BP.
XX
AC ACC85276;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 2 gene.
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003050287-A2.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX

(SCHM/) SCHMULLING T.
(WERN/) WERNER T.
Schmullling T, Werner T;
WPI; 2003-541577/51.
P-PSDB; ABR63569.
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 3; Page 145-146; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence

CC shown in the invention
XX
SQ Sequence 2991 BP; 920 A; 522 C; 521 G; 1028 T; 0 U; 0 Other;
Alignment Scores: 1.06e-225 Length: 2991
Pred. No.: 2226.50 Matches: 499
Score: 2226.50
Percent Similarity: 50.00% Conservative: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 85.77% Indels: 499
DB: 8 Gaps: 4
US-10-014-101-4 (1-501) x ACC85276 (1-2991)
QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20
Db 1 ATGGCTAATCTTCGTTTAAATGATCACTTTAATCACGGTTTAAATGATCACCAATCATCA 60
QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40
Db 61 AACGGTATTAAATTGATTTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC 120
QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
Db 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATAAACCCGTGACCCCGCGGCGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80
Db 181 ATCTGCCCTCTCTCCACCGCTGATATCTCTCGTCTCTCCAATACGCCGCAACGGAAAA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
Db 241 AGTACATTCCAAGTAGCGGCTCGTGCCCAAGGCCACTCTCTTAAACGGCCACCGCTCG 300
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValSerLysAspLys 120
Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAGACAG 360
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGlu 140
Db 361 AAGTACGCTGACGTGGCGCGGACGTTATGGTGGATGTCTTAAAGAAGACGGCGGAG 420
QY 141 LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160
Db 421 AAAGGGGTGTCGCCGGTTTCTTGGACGGATTATTTGCATATAAACCGTCGGAGGAACGTTG 480
QY 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180
Db 481 TCGAATGGTGAATTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACGTCCTT 540
QY 181 GluLeuAspValIleThr----- 186
Db 541 GAATTGGACGTTATTACTGGTACGCATCTTCTAAACTTTTGATGTACATACAACAACAAA 600
QY 186 ----- 186
Db 601 ACTGTTTTTGTATTATAGTATTTTTCATTTTGTACCATAGGTTTATGTTTATAGTT 660
QY 186 ----- 186
Db 661 GTGCTAAACTCTTGCACCACACGTAAGTCTTCGAAACACAAAATGCGTAACGCATCTAT 720
QY 186 ----- 186
Db 721 ATGTTTTTTGTACATATTGAATGTTGTTCATGAGAAATAAAGTAATTACATATACACACA 780
QY 186 ----- 186
Db 781 TTTATTGTCGTACATATATAATAATAATAAGACAAATTTTCACAAATTGGTAGCGTTAA 840
QY 186 ----- 186
Db 841 TTGGGATTTTGTAAATGTACATGCATGACGCGCATGATGGAGCTTTTCGGTTTCTTA 900

QY 186 ----- 186
Db 901 GATTGTGTAGTATTTCAAATATATCATTTATTTCTTTCGAATAAAGAGTGGTATATT 960
QY 186 ----- 186
Db 961 TTTAAATAGCAACATTTTCAGAAATTTTCTTTGAATTTACACTTTTAAATGTTATTGT 1020
QY 187 -----GlyLysGlyGluMetLeuThrCysSerArgG1 197
Db 1021 TAATATGGATTTTGAATAAATAATTTTCAGGGAAGGTGAAATGTTGACATGCTCGCGACA 1080
QY 197 nLeuAsnProGluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleTh 217
Db 1081 GCTAAACCCAGAAATGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAATTATAAC 1140
QY 217 rArgAlaArgIleValLeuAspHisAlaProLys----- 228
Db 1141 GAGAGCCAGAATTGTTTGGACCATGCACCTAAACGGGTACGTATCATCATATTTTACCA 1200
QY 228 ----- 228
Db 1201 TTTGTTTGTAGTCAGCAATTCATTTTTCATTAGTAATTCGGTTTTCAAATTTCTAAATTTTTT 1260
QY 228 ----- 228
Db 1261 AGTCAATAGAAAATGATTTCTTATGTCAGAGCTTGATTTATTAGTGATTTTATTGAGATA 1320
QY 228 ----- 228
Db 1321 AAATAAAATATAACCTAACCGAAATAATATTTTACTAATCGGATAATGTCGTGATTAAAA 1380
QY 228 ----- 228
Db 1381 CATTTTATGATATTACACTAAGAGAGTTAGAGACGTATGGATCACAAAACATGAAGCTTT 1440
QY 228 ----- 228
Db 1441 CTTAGATGGTATCCTAAACCTAAAGTTAGGTACAAAGTTTGGAAATTTAGGTCAATGCTTA 1500
QY 228 ----- 228
Db 1501 AGTTGCATTAATTTGAACAAATCTATGCATTTGAATAAAAAAAGATATGGATTATTTTA 1560
QY 228 ----- 228
Db 1561 TAAAGTATAGTCTTGTGTAATCCTAGGACTTGTGTCTAATCTTGTCTTATGCGTGCAAAAT 1620
QY 228 ----- 228
Db 1621 CTTTTTGATGTCAATATATAATCCTGTTTATTAGAGTCAAGCTCTTTTCATTAGTCAACT 1680
QY 228 ----- 228
Db 1681 ACTCAATATACTCCAAAGTTTAGAATATAGTCTTCTGACTAATTAGAATCTTTACAACCG 1740
QY 228 ----- 228
Db 1741 ATAAACGTTACAATTTGGTTATCAFTTTAAAAAACAGATTTGGTCATAATATACGATGAC 1800
QY 228 ----- 228
Db 1801 GTTCTGTTTGTAGTTTCACTATTTCACAAATTTTATATAATTAATTTTCAAGAAAAATATTGA 1860
QY 228 ----- 228
Db 1861 AATACTATACTGTAATATGGTTTCTTTATATATATGTGTGTATATAAATAATGGGATTGTTT 1920
QY 229 -----ArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrTh 242
Db 1921 TCTCTAAATGAAATTTGTGTAGGCC-AAATGGTTTCGGATGCTCTACAGTGATTTTCACAAC 1979

QY 242 rPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLe 262
Db 1980 TTTTACAAAGGACCAGAACGTTTGATATCAATGSCAAACGATATTGGAGTGCACATATT 2039
QY 262 uGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAs 282
Db 2040 ABAAGGTCAAATATTTCTATCAAACGGTGTGTTGACACCTCTTTTTCACACCTTCAGA 2099
QY 282 pGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAl 302
Db 2100 TCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGCTATCATCTATGTTCTTGAAGTAGC 2159
QY 302 aLysTyrTyrAspAspProAsnLeuProIleIleSerLys----- 315
Db 2160 CAAGTATTATGATGATGCCAATCTCCCATCATCAGCAAGGTACTACACATTTACATTTT 2219
QY 315 ----- 315
Db 2220 CATCATCGTTTTTATCATACCATAAGATATTTAAATGATTTCATTCATTCACCACATTAAG 2279
QY 315 ----- 315
Db 2280 ATATTTCATCATCATCGTTACATTTTTTTTTTGGCATCTTATGCTTCTCATAATCTACTA 2339
QY 316 -----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerM 333
Db 2340 TTGTGTAGGTTATTGACACATTAACGAAACATTAAAGTTACTTGGCCGGGTTCATATCAA 2399
QY 333 etHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuA 353
Db 2400 TGCACGACGTGGCCTACTTCGATTTCTTGAACCGTGTACATGTCGAAGAAATAAACTCA 2459
QY 353 rgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSera 373
Db 2460 GATCTTTGGGATTATGGGAACCTCCTCATCCTTGGCTTAACCTCTACGTTCCCTAAATCTC 2519
QY 373 rgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAlaS 393
Db 2520 GGATTTCTCGATTTTTCATAACGGTGTGTCAAAGACATTTCTTCTTAAGCAAAATCAGCTT 2579
QY 393 erGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405
Db 2580 CGGGACTCGCTCTTCTCTATCCAAACAAACCGGAATAA-GTACATACTTCTCTTCATTCA 2638
QY 405 ----- 405
Db 2639 ATTTATCTTCAAGAACCAAGTAATAAATTTCTATGAACCTGATTATGCTGTTATTGTTA 2698
QY 406 --TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleI 425
Db 2699 GATGGGACAAATCGTATGTGCGCGATGATACAGAGATCGATGAAGATGTTATATATATA 2758
QY 425 leGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluL 445
Db 2759 TCGGACTACTACAATCCGCTACCCCAAAGGATCTTCCAGAACTGGAGAGCGTTAACGAGA 2818
QY 445 ysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrT 465
Db 2819 AGATAATTAGGTTTTCGAAGGATTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATA 2878
QY 465 hrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArgL 485
Db 2879 CTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGA 2938
QY 485 ysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 2939 AAGATCTATTGATCCCAAGAAACCTGTATCTCTCCAGGGCAAGACATCTTTT 2988

RESULT 6

AAC42983
ID AAC42983 standard; DNA; 1575 BP.
XX
AC AAC42983;

XX 17-OCT-2000 (first entry)
DT Arabidopsis thaliana DNA fragment SEQ ID NO: 37588.
XX
DE
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.


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QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1285 TGGAAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTATGTATC 1338

QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTGGCAAGAACTTGAAATCTCAACGAC 1398

QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1399 AAGGTATTTCAGTTTGTGAAAACTCGGGAATTAGATTAAAGGAATATTATGATGCACTAT 1458

QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTyrAspAspPheSerLysArg 484
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1459 ACAAGAAAAGAAAGATTGGGTTAAACATTTTGGACCAAAATGGGATGATTTTAAAGAAAG 1518

QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1519 AAAATTATGTTTGATCCCAAAAGACTATTGTCTCCAGGACAAGACATATTT 1569
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RESULT 7
ABZ14284
ID ABZ14284 standard; DNA; 1575 BP.

XX ABZ14284;
AC
XX
DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2089.
DE
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
KW

XX Arabidopsis thaliana.
OS
XX
PN WO200216655-A2.

XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.

XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.

XX
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
DR WPI; 2002-304127/34.

XX
PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 2089; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office

XX Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 3.78e-183 Length: 1575

```
Score: 1822.00 Matches: 345  
Percent Similarity: 80.08% Conservative: 69  
Best Local Similarity: 66.73% Mismatches: 79  
Query Match: 70.18% Indels: 24  
DB: 6 Gaps: 5  
US-10-014-101-4 (1-501) x ABZ14284 (1-1575)  
QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 25 CTCATCACCCCTAATAACCGCTTTTATAAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 85 GGCAATGATGTTTCTTACCATATCACTCAACCTTACGGTCTCTAACCGATCCCTTCTCTCC 144  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 145 ATCTCTGCCGCTTCTCACGACTTCGGTAACATAACCGACGAAATCCCGGCGCGCTCTC 204  
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QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 205 TGCCCTTCCTCCACCACCGAGGTGGTCTGCTCTCCTCCGTTCCGTTAACGGAGGATTTCTCT 264  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 265 TACAATAAAGGCTCAACACCGCCCGCGTCTACTTTTCAAGTGGTCTGCTCGAGGCCAAGGC 324  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 325 CACTCCCTCCGTGGCCAAAGCCTCTGCACCCGAGGTGTCGTGTAACATGACGTGTCTC 384  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 112 -----ThrAspValValSerLysAspLysLysTyrAlaAspVal 125  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 385 GCCATGGCGGCTAAACACCGCGCGGTGTTATCTCGGCAGACGGGACTTACGCTGACGTG 444  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 445 GCTGCCGGGACGATGTGGTGGATGTTCTGAAGCGCGCGGTGGATAGAGCGCTCTCGCCG 504  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165  
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Db 505 GTTACATGGACGGATTATTTGTATCTCAGCGTCCGCGGGACGTTGTCTGAAACGCTGGAATC 564  
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QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185  
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Db 565 GGTGGTCAGACGTTTAGACACGCGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTTATT 624  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 625 ACCGAAAAGGTGAAATGATGACTTGCTCTCCAAAGTTAAACCCCTGAATTTCTTCTATGA 684  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 206 ValLeuGlyGlyLeuGlnPheGlyIleIleThrArgAlaAlaArgIleValLeuAspHis 225  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 685 GTTTTAGGAGGTTTGGTCAATTTCGGTATTATTAACGAGGGCCAGGATTGCGTTGGATCAT 744  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrThrLys 245  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 745 GCACCCACAAGGTTGAAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA 804  
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QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGln 265  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTGGAGGTCAA 864  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTTCTCCCACTCTCCGATCAACAAGA 924  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 925 GTCGCATCTCTTGTGAATGACCAACCGGATCATCTATGTTCTCGAAGTAGCCAAGTATTAT 984  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 306 AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer 325
```


DB 985 GACAGAACCCCTTCCCATTTATGACCAGGTGATTGACACGTTAAGTAAAGTAACTAGGT 1044

QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345

DB 1045 TTGCGTCCAGGGTTATGTTTCGTACAAGATGTTCCGTATTTCGATTCTTGAACCGTGTG 1104

QY 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrPheGluLeuProHisProTyrLeu 365

DB 1105 CGAAACGAAGAATAAACTCAGATCTTTAGGACTATGGGAAGTTCCTCATCCATGGCTT 1164

QY 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385

DB 1165 AACATCTTTGTCGGGGTCTCGAATCCAAGATTTTCATGATGGTGTATTAAATGGCCTT 1224

QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405

DB 1225 CTTCTAAACCAACCTCAACTTCTGGTGTACTCTTCTTATCCCAACCAACCGAACA 1284

QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425

DB 1285 TCGAACCAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTATGTGATC 1338

QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444

DB 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTCGCAAGAACTTGAAATCTCAACGAC 1398

QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464

DB 1399 AAGTTATTTCAGTTTTGTGAAAACCTCGGGAATTAAGATTAAGGAATATTGATGCACTAT 1458

QY 465 ThrSerLysGluAspTyrIleGluHisPheGlySerLysTyrAspAspPheSerLysArg 484

DB 1459 ACAAGAAAAGAGAGATTGGGTTAAACATTTTGGACCAAAATGGGATGATTTTTTAAGAAAG 1518

QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501

DB 1519 AAAATPATGTTTGATCCCAAAAGACTATTGTCTCCAGGACAAGACATATTT 1569

RESULT 8

ABK28627

ID ABK28627 standard; cDNA; 1575 BP.

XX AC ABK28627;

XX DT 09-APR-2002 (first entry)

XX DE cDNA encoding A. thaliana cytokinin oxidase AtCKX4.

XX KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;

XX KW root growth; lateral root; adventitious root; root geotropism; herbicide;

XX KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.

XX OS Arabidopsis thaliana.

XX PN WO200196580-A2.

XX PD 20-DEC-2001.

XX PF 18-JUN-2001; 2001WO-EP006833.

XX PR 16-JUN-2000; 2000EP-00870132.

XX PR 27-DEC-2000; 2000US-0258415P.

XX PR 16-MAR-2001; 2001EP-00870053.

XX PA (SCHM/) SCHMULLING T.

XX PA (WERN/) WERNER T.

XX PI Schmulling T, Werner T;

XX DR WPI; 2002-130736/17.

XX PT Polynucleotide encoding novel plant protein having cytokinin oxidase

PT activity and the protein useful for stimulating root growth, enhancing

PT the formation of lateral or adventitious roots, altering root geotropism.

XX Claim 2; Page 147-148; 154pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding a novel

CC plant protein (II) having cytokinin oxidase activity. (I) is useful for

CC production of transgenic plants, plant cells or tissues; for production

CC of altered plants, plant cell or tissues; and for effecting the

CC expression of (II) where (I) is operably linked to one or more control

CC sequences. The methods further comprises regenerating a plant from the

CC plant cell. (I) and (II) are useful for stimulating root growth;

CC enhancing the formation of lateral or adventitious roots; altering root

CC geotropism, leading to an increase in yield; and for screening growth

CC promoting chemical of herbicides. (I) is useful for increasing the size

CC of the root meristem; increasing root size; increasing the size of the

CC shoot meristem; delaying leaf senescence and altering leaf senescence;

CC increasing leaf thickness; reducing or increasing the vessel size;

CC inducing parthenocarp; improving standability of the seedlings;

CC increasing branching and for improving lodging resistance. Antibody (III)

CC to (II) is useful for identifying and obtaining proteins interacting with

CC (II) comprising a screening assay, preferably a two-hybrid screening

CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase

CC coding sequences and PCR primers of the invention

XX Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 3.78e-183 Length: 1575

Score: 1822.00 Matches: 345

Percent Similarity: 80.08% Conservative: 69

Best Local Similarity: 66.73% Mismatches: 79

Query Match: 70.18% Indels: 24

DB: 6 Gaps: 5

US-10-014-101-4 (1-501) x ABK28627 (1-1575)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21

DB 25 CTCATCACCCCTAATAACGCTTTTATATAAGTTTAAACCCCAACCTTAATCAAATCAGATGAG 84

QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41

DB 85 GGCATTGATGTTTCTTACCCATATCACTCAACCTTACGGTCTTAACCGATCCCTTCTCC 144

QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61

DB 145 ATCTCTGCGCTTCTCACGACTTCGTTAAACATAACCGACGAAATCCCGCGCTCTC 204

QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79

DB 205 TGCCCTTCCTCCACCAACGAGGTGGCTCGTCTCTCCGTTTCGCTAACCGAGGATTTCT 264

QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91

DB 265 TACAATAAAGGCTCAACCAAGCCCGCTCTACTTTCAAAGTGGCTCGAGGCCAAGGC 324

QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111

DB 325 CACTCCCTCCGTGGCCCAAGCCTCTGCACCCGAGGTGTCTGCTGTAACATGACGTGTCTC 384

QY 112 -----ThrAspValValSerLysAspLysLysTyrAlaAspVal 125

DB 385 GCCATGGCGGCTAAACCAAGCGGCTGTATCTCGGCAGACGCGGACTTACGCTGACGTG 444

QY 126 AlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145

DB 445 GCTGCCGGGACGATGTGGTGGATGTTCTGAAGCGCGGTGGATAGAGCGGTCTCGCCG 504

QY 146 ValSerTyrThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165

DB 505 GTTACATGGACGGATTATTTGTATCTCAGCGTCGGCGGACGTTGTTCGAACCGTGGATC 564

Qy	166	GlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValile	185
Db	565	GGTGGTCAGACGTTTAGACACGGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTTATT	624
Qy	186	ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly	205
Db	625	ACCGGAAAAGGTGAATGATGACTTGCTCTCCAAAGTTAAACCCCTGAATTGTTCTATGGA	684
Qy	206	ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis	225
Db	685	GTTTTAGGAGGTTTGGGTCAATTCCGGTATTATAACGAGGGCCAGGATTGCGTTGGATCAT	744
Qy	226	AlaProLysArgAlaLysTirPheArgMetLeuTyrSerAspPheThrThrPheThrLys	245
Db	745	GCACCCACAAGGTGAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA	804
Qy	246	AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGln	265
Db	805	GACCAAGAGCGTTTAATCAATGACCAATGATCTCGAGTTGACTTTTGGAAAGGTCAA	864
Qy	266	IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys	285
Db	865	CTTATGATGTCAAAATGGCTTCGTAGACACCTCTTTCTCCCACTCTCCGATCAACAAGA	924
Qy	286	ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr	305
Db	925	GTCGCATCTCTTGTAATGACCAACCGGATCATCTATGTTCTCGAAGTAGCAAGTATTAT	984
Qy	306	AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer	325
Db	985	GACAGAACCAACCTTCCCATTATTGACCAGGTGATTGACACGTTAAGTAGAACTCTAGGT	1044
Qy	326	TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal	345
Db	1045	TTCGCTCCAGGGTTATGTTCCGTACAAGATGTTCCGTATTTTCGATTTCTTGAAACCGTGC	1104
Qy	346	HisValGluGluAsnLysLeuArgSerLeuGlyLeuTirPLeuLeuProHisProTirPLeu	365
Db	1105	CGAAACGAAGAAGATAAACTCAGATCTTTAGGACTATGGGAAGTTCCCTCATCCATGGCTT	1164
Qy	366	AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle	385
Db	1165	AACATCTTTGTCCGGGTCTCGAATCCAGATTTTCATGATGGTGTATTATTAATGGCCTT	1224
Qy	386	LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys	405
Db	1225	CTTCTAAACCAACCTCAACTTCTGGTGTTACTCTCTTATCCCAACCAACCGAAACAAA	1284
Qy	406	TirPAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle	425
Db	1285	TGGAACAACCGCATGTCACGATGACACCG-----GACGAAGATGTTTTTTATGTGATC	1338
Qy	426	GlyLeuLeuGlnSerAla--ThrProLysAspLeuProGluValGluSerValAsnGlu	444
Db	1339	GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAAATCTCAACGAC	1398
Qy	445	LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMethHisTyr	464
Db	1399	AAGGTTATTTCAGTTTTGTGAAAACCTCGGAATTAAAGGATATTATTGATGCACTAT	1458
Qy	465	ThrSerLysGluAspTirPleGluHisPheGlySerLysTirPAspAspPheSerLysArg	484
Db	1459	ACAAGAAAAGAAGATTGGGTTAAACATTTTGGACCAAAATGGGATGATTTTTTTAAGAAG	1518
Qy	485	LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe	501
Db	1519	AAAATTATGTTGATCCCAAAAGACTATTGTTCTCCAGGACAAGACATATTT	1569

RESULT 9

ADA68648

ID ADA68648 standard; DNA; 1575 BP.

XX

AC ADA68648;

XX	20-NOV-2003	(first entry)
XX	DT	
XX	XX	
DE	Arabidopsis thaliana	gene, SEQ ID 428.
XX	XX	
XX	KW	plant; bacterial infection; fungal infection; viral infection; ds.
XX	XX	
OS	Arabidopsis thaliana.	
XX	XX	
PN	WO2003000898-A1.	
XX	XX	
PD	03-JAN-2003.	
XX	XX	
PF	22-JUN-2001; 2001WO-IB001105.	
XX	XX	
PR	22-JUN-2001; 2001WO-IB001105.	
XX	XX	
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.	
XX	XX	
PI	Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;	
PI	Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;	
XX	XX	
DR	WPI; 2003-175290/17.	
XX	XX	
PT	Identifying at least one gene involved in plant resistance or response to	
PT	pathogenic infection for conferring resistance or tolerance to a plant to	
PT	bacterial, fungal or viral infection by determining or detecting plant	
PT	gene expression.	
XX	XX	
PS	Claim 6; SEQ ID NO 428; 899pp; English.	
XX	XX	
CC	The present invention relates to a method (M1) for identifying genes	
CC	involved in plant resistance or response to pathogenic infection. M1	
CC	comprises identifying a gene whose expression is significantly altered in	
CC	the incompatible interaction of plant gene expression relative to	
CC	expression of the gene in an uninfected plant, in a mutant plant that	
CC	does not express a gene associated with response to pathogenic infection,	
CC	or in a corresponding incompatible or compatible interaction. (M1) is	
CC	useful for conferring resistance to resistance or tolerance to a plant to	
CC	bacterial, fungal or viral infection. The present sequence was used to	
CC	illustrate the invention.	
XX	XX	
SQ	Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;	
XX	XX	
Alignment Scores:		
Pred. No.:	3.78e-183	Length: 1575
Score:	1822.00	Matches: 345
Percent Similarity:	80.08%	Conservative: 69
Best Local Similarity:	66.73%	Mismatches: 79
Query Match:	70.18%	Indels: 24
DB:	7	Gaps: 5
XX	XX	
US-10-014-101-4	(1-501) x ADA68648 (1-1575)	
QY	7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21	
DB	25 CTCATCACCCCTAATAACGCTTTTATAAGTTTAACCCCAACCTTAATCAAATCAGATGAG 84	
QY	22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41	
DB	85 GGCATTGATGTTTTCTTACCCATATCACTCAACCTTACGGTCTCTAACCAGTCCCTTCTCC 144	
QY	42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61	
DB	145 ATCTCTGCCGCTTCTCACGACTTCGGTAACATAACCGACGAAATCCCGCGCGCTCCTC 204	
QY	62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79	
DB	205 TGCCCTTCTCTCCACCACCGAGGTGGCTCGTCTCCTCCGTTTCGTTAACGGAGGATTCTCT 264	
QY	80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91	
DB	265 TACAATAAAGGCTCAACCGCCCGCTCTACTTTCAAAGTGGCTGCTCGAGGCCAAGGC 324	

QY	92	HisSerLeu	AsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle	111
DB	325	CAC	TCCCTCCGTGGCCAAAGCCTCTGCACCCGAGGTGTCGTCGTGAACATGACGTGTCTC	384
QY	112	-----	-----ThrAspValValValSerLysAspLysLysTyrAlaAspVal	125
DB	385	GCCATGGCGCGCTAAAC	CAGCGCGTGTGTTATCTCGGCAGACGGGACTTACGCTGACGTG	444
QY	126	AlaAlaGlyThrLeu	TrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro	145
DB	445	GCTGCCGGGACGATGTGGGTGGATGTTCTGAAGCGCGGTGGATAGAGGCGTCTGCCCG	504	
QY	146	ValSerTrpThrAspTyrLeu	HisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle	165
DB	505	GTTACATGGACGGATTATTTGTATCTCAGCGTCGGCGGGACGTTGTGCGAACGCTGGAATC	564	
QY	166	GlyGlyGlnValPheArgAsn	GlyProLeuValSerAsnValLeuGluLeuAspValIle	185
DB	565	GGTGGTCAGACGTTTAGACACGCGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTTATT	624	
QY	186	ThrGlyLysGlyGluMetLeu	ThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly	205
DB	625	ACCGAAAGGTGAATGATGACTTGCTCTCCAAAGTTAAACCCCTGAATTGTTCTATGGA	684	
QY	206	ValLeuGlyGlyLeuGlyGlnPhe	GlyIleIleThrArgAlaArgIleValLeuAspHis	225
DB	685	GTTTTAGGAGGTTGGGTCAATTCCGTTATTATAACGAGGGCCAGGATTGCGTTGGATCAT	744	
QY	226	AlaProLysArgAlaLysTrpPhe	ArgMetLeuTyrSerAspPheThrThrPheThrLys	245
DB	745	GCACCCCAAGGTCGAAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA	804	
QY	246	AspGlnGluArgLeuIleSerMet	AlaAsnAspIleGlyValAspTyrLeuGluGln	265
DB	805	GACCAAGAGCGTTAATATCAATGACCAATGATCTCGAGTTGACTTTTGGAGGTCAA	864	
QY	266	IlePheLeuSerAsnGlyValVal	AspThrSerPhePheProProSerAspGlnSerLys	285
DB	865	CTTATGATGTCAAATGGCTTCGTAGACACCTCTTCTCCACTCTCCGATCAACAAGA	924	
QY	286	ValAlaAspLeuValLysGlnHis	GlyIleIleTyrValLeuGluValAlaLysTyrTyr	305
DB	925	GTCGCATCTCTTGTAATGACCAACCGGATCATCTATGTTCTCGAAGTAGCCAACTATTAT	984	
QY	306	AspAspProAsnLeuProIleIle	SerLysValIleAspThrLeuThrLysThrLeuSer	325
DB	985	GACAGAACCCCTTCCCATATTATGACCAGGTGATGACACGTTAAGTAGAAGTCTAGGT	1044	
QY	326	TyrLeuProGlyPheIleSerMet	HisAspValAlaTyrPheAspPheLeuAsnArgVal	345
DB	1045	TTCGCTCCAGGGTTATGTTGTCACAAGATGTTCCGTATTTTCGATTCTTGAACCGGTGC	1104	
QY	346	HisValGluGluAsnLysLeuArg	SerLeuGlyLeuTrpGluLeuProHisProTrpLeu	365
DB	1105	CGAAACGAAGAAGATAAACTCAGATCTTTAGGACTATGGGAAGTTCTCTCATCCATGGCTT	1164	
QY	366	AsnLeuTyrValProLysSerArg	IleLeuAspPheHisAsnGlyValValLysAspIle	385
DB	1165	AACATCTTTGTCCCGGGTCTCGAATCCAAAGATTTTCATGATGGTGTATTATATGGCCTT	1224	
QY	386	LeuLeuLysGlnLysSerAlaSer	GlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys	405
DB	1225	CTTCTAAACCAACCTCAACTTCTGGTGTACTCTCTTCTATCCCAACCGAACAACAA	1284	
QY	406	TrpAspAsnArgMetSerAlaMet	IleProGluIleAspGluAspValIleTyrIleIle	425
DB	1285	TGGAACAACCGCATGTCAACGATGACACCG	-----GACGAAGATGTTTTTTATGTGATC	1338
QY	426	GlyLeuLeuGlnSerAla	---ThrProLysAspLeuProGluValGluSerValAsnGlu	444
DB	1339	GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTTGAAATCTCAACGAC	1398	

Qy	445	LysIlelleArgPheCysLysAspSerGlyIleLysLeuLysGlnTyrIleuMetHisTyr	464
Db	1399	AAGGTTATTCAGTTTTGTGAAACCTCGGAATTAAAGATTAAAGGAATAATTGATGCACATAT	1458
Qy	465	ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg	484
Db	1459	ACAAGAAAAGAAGATTGGGTTAAACATTTTGACC AAAATGGGATGATTTTTTAAGAAAG	1518
Qy	485	LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe	501
Db	1519	AAAATTATGTTGATCCCAAAGACTATGTCTCCAGGACAAGACATATTT	1569
 RESULT 10 ACC85296			
ID	ACC85296	standard; cDNA; 1575 BP.	
XX	AC		
XX	ACC85296;		
DT	18-SEP-2003	(first entry)	
XX			
DE	Arabidopsis cytokinin oxidase-like protein 4 cDNA.		
XX			
KW	Maize; root growth; root geotropism; cytokinin oxidase; seed size;		
KW	embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	WO2003050287-A2.		
XX			
PD	19-JUN-2003.		
XX			
PF	10-DEC-2002; 2002WO-EP013990.		
XX			
PR	10-DEC-2001; 2001US-00014101.		
XX			
PA	{SCHM/} SCHMULLING T.		
PA	{WERN/} WERNER T.		
XX			
PI	Schmullling T, Werner T;		
XX			
DR	WPI; 2003-541577/51.		
XX			
PT	Stimulating root growth, enhancing lateral or adventitious root formation		
PT	or altering root geotropism comprises increasing plant cytokinin oxidase		
PT	levels or other protein or nucleic acid that reduces active cytokinins in		
PT	a plant.		
XX			
PS	Claim 2; Page 169-170; 177pp; English.		
XX			
CC	The present invention relates to a method for stimulating root growth or		
CC	enhancing the formation of lateral or adventitious roots or altering root		
CC	geotropism, which comprises increasing in a plant or plant part the level		
CC	of a plant cytokinin oxidase or other protein that reduces the level of		
CC	active cytokinins in a plant or plant part. Cytokinin oxidase protein and		
CC	coding sequences from Arabidopsis thaliana are also provided. The method		
CC	is useful in modifying plant morphological, biochemical and physiological		
CC	properties, such as in modifying the initiation, stimulation or		
CC	enhancement of root growth, adventitious root formation, lateral root		
CC	formation, root geotropism, shoot growth, apical dominance, branching,		
CC	timing of senescence, timing of flowering, flower formation, seed		
CC	development and/or seed yield. The present sequence is a coding sequence		
CC	shown in the invention		
XX			
SQ	Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;		

Alignment Scores:		
Pred. No.:	3.78e-183	1575
Score:	1822.00	345
Percent Similarity:	80.08%	69
Best Local Similarity:	66.73%	79
Query Match:	70.18%	24
DB:	8	5
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-10-014-101-4 (1-501) x ACC85296 (1-1575)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
Db 25 CTCATCACCCCTAATAACGCTTTTATAGTTTAAACCCCAACCTTAAATCAATCAGATGAG 84

QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
Db 85 GGCATTGATGTTTCTTACCCATATCACTCAACCTTACGGTCTCTAACCGATCCCTTCTCC 144

QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrValThrProGlyGlyValIle 61
Db 145 ATCTCTGCCGCTTCTCACGACTTCGGTAACATAACCGACGAAATCCCGCGCGCTCCTC 204

QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
Db 205 TGCCCTTCTCCACCACGGAGGTGGCTCGTCTCCCTCGTTTCGCTAACGGAGGATTCTCT 264

QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db 265 TACAATAAAGGCTCAACCCAGCCCGCGTCTACTTTCAAAGTGGTCTCGTCCAGGCCAAGGC 324

QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
Db 325 CACTCCCTCCGTGGCCCAAGCTCTGCACCCGGAGGTGCTGCTGTAACATGACGTGTCTC 384

QY 112 -----ThrAspValValValSerLysAspLysLysTyrAlaAspVal 125
Db 385 GCCATGGCGGCTAAACCCAGCCGCGTGTATTATCTCGGCAGACGGGACTTACGTGACGTG 444

QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145
Db 445 GCTGCCGGGACGATGTGGGTGGATGTTCTGAAGCGCGGGTGGATAGAGGCGTCTCGCCG 504

QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
Db 505 GTTACATGGACGGATTATTTGTATCTCAGCGTGGCGGGAGCGTTGTGCAACGCTGGAATC 564

QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185
Db 565 GGTGTGTAGACGCTTTAGACACGGCCCTCAGATTAGTAACTTATGAGCTTGAGCTTATT 624

QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205
Db 625 ACCGAAAAGGTGAAATGATGACTTGCTCTCCAAAGTTAAACCCCTGAATTGTTCTATGGA 684

QY 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225
Db 685 GTTTTAGGAGGTTTGGGTCAATTCCGTATTATAACGAGGCGCAGGATTGCGTTGGATCAT 744

QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245
Db 745 GCACCCACAAAGGTTGAAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA 804

QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGln 265
Db 805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTGGAAAGTCAA 864

QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285
Db 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTTCTTCCCACTCTCCGATCAACAAGA 924

QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305
Db 925 GTCGCATCTCTGTGAATGACCAACCGGATCATCTATGTTCTCGAAGTAGCCAAGTATTAT 984

QY 306 AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer 325
Db 985 GACAGAACCCCTTCCCATTTATTGACCAAGGTGATTGACACGTAAAGTAGAACTCTAGGT 1044

QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345
Db 1045 TTCGCTCCAGGTTTATGTTGCTACAAAGATGTTCCGTATTTCGATTCTTGAACCCGTGTC 1104

QY 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365
Db 1105 CGAAACGAAGAAGATAAATCAGATCTTTAGGACTATGGGAAGTTCTCTCATCCATGGCTT 1164

QY 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385
Db 1165 AACATCTTTGTCCCGGGTCTCGAATCCAAGATTTTCATGATGGTGTATTATTAATGGCCTT 1224

QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405
Db 1225 CTTCTAAACCAACCTCAACTTCTGGTGTACTCTCTTATCCCAACAAACCGAAACAAA 1284

QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425
Db 1285 TGGAAACAACCGCATGTCTACAGATGACACCG-----GACGAAGATGTTTTTATGTGATC 1338

QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAATCTCAACGAC 1398

QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db 1399 AAGGTATTTCAGTTTTTGAAAACTCGGGAATTAAGATTAAGGAATATTGTGACACTAT 1458

QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484
Db 1459 ACAAGAAAAGAGATTGGGTAAACATTTTGGACCACCAAAATGGGATGATTTTTTAAGAAAG 1518

QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1519 AAAATTATGTTTGTATCCCAAGAACTATTGTCTCCAGGACAAGACATATTT 1569

RESULT 11
ABK28609
ID ABK28609 standard; DNA; 2782 BP.
XX
AC ABK28609;
XX
DT 09-APR-2002 (first entry)
XX
DE DNA encoding A. thaliana cytokinin oxidase AtCKX4.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocary; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmulling T, Werner T;
XX
DR WPI; 2002-130736/17.
DR P-PSDB; AAU81970.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 134-135; 154pp; English.
XX

The invention relates to an isolated polynucleotide (I) encoding a novel plant protein (II) having cytokinin oxidase activity. (I) is useful for production of transgenic plants, plant cells or tissues; for production of altered plants, plant cell or tissues; and for effecting the expression of (II) where (I) is operably linked to one or more control sequences. The methods further comprises regenerating a plant from the plant cell. (I) and (II) are useful for stimulating root growth; enhancing the formation of lateral or adventitious roots; altering root geotropism, leading to an increase in yield; and for screening growth promoting chemical of herbicides. (I) is useful for increasing the size of the root meristem; increasing root size; increasing the size of the shoot meristem; delaying leaf senescence and altering leaf senescence; increasing leaf thickness; reducing or increasing the vessel size; inducing parthenocarp; improving standability of the seedlings; increasing branching and for improving lodging resistance. Antibody (III) to (II) is useful for identifying and obtaining proteins interacting with (II) comprising a screening assay, preferably a two-hybrid screening assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase coding sequences and PCR primers of the invention

Db 1703 TCAATGACCAATGATCTCGAGTTGACTTTTGGAGGTCAACTTATGATGTCAAATGGC 1762
QY 272 ValValAspThrSerPheProProSerAspGlnSerLysValAlaAspLeuVallys 291
Db 1763 TTCGTAGACACCTCTTCTCCACTCTCCGATCAACAAGAGTGCATCTCTGTGAAT 1822
QY 292 GlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsnLeuPro 311
Db 1823 GACCACCGGATCATCTATGTTCTCGAAGTAGCCCAAGTATATGACAGAACCACCTTCCC 1882
QY 312 IleIleSerLys----- 315
Db 1883 ATTATTGACCAGGTACTATAATCCATTATTTCATGATGATTATCTTCACACAATCAGTATC 1942
QY 315 ----- 315
Db 1943 ATCACCAAATTACCATCATCACTTGTTCATATATGATCCAAAGTAAATATATCATCATGATAT 2002
QY 315 ----- 315
Db 2003 AAATAAATCGTTCAAATCTTTTTTTTAAAGATAATAAAGAAATCATTTTCAAGCATTAATC 2062
QY 315 ----- 315
Db 2063 ATACACATCTACGAATCACCGTGACCATATATAACCATACGCTTATTAAATAATCATTTT 2122
QY 316 -----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSer 332
Db 2123 TGTGTTGAGGTGATTGACACGTTAAGTAGAACTCTAGGTTTCGCTCCAGGGTTTATGTTTC 2182
QY 333 MetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeu 352
Db 2183 GTACAAGATGTTCCGTATTTTCGATTCTTGTGAACCGTGTCGAAACGAGAAGATAAACTC 2242
QY 353 ArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSer 372
Db 2243 AGATCTTTAGGACTATGGGAAGTTCTCTCATCCATGGCTTAACATCTTTGTCCCGGGTCT 2302
QY 373 ArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAla 392
Db 2303 CGAATCCAGATTTTTCATGATGGTGTTATTAAATGGCCTTCTTAAACCAACCTCAACT 2362
QY 393 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405
Db 2363 TCTGGTGTACTCTCTCTATCCCAACAAACCGAAACAAAGTAAATATTTACTTTTGTGATT 2422
QY 405 ----- 405
Db 2423 TGTTTTATTGAAAGTATATATCCCAATAATGTATGTTAAATGTTAAACAAGATTTATTTT 2482
QY 406 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIle 422
Db 2483 ATTAATAGATGGAAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTT 2536
QY 423 TyrIleIleGlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSer 441
Db 2537 TATGTGATCGGATTACTGCAATCAGTGTGGATCTCATAAATTGGCAAGAACTTGAAAT 2596
QY 442 ValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeu 461
Db 2597 CTCAACGACAAAGTTATTTCAGTTTGTGAAAACCTCGGGAATTAAGATTAAAGGAATATTG 2656
QY 462 MetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPhe 481
Db 2657 ATGCACTATACAGAAAAGAAGATTGGGTTAAACATTTTGGACCAAAATGGGATGATTTT 2716
QY 482 SerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 2717 TTAAGAAAGAAAATTATGTTGATCCCAAAAGACTATTGTCTCCAGGACAAGACATATT 2776

RESULT 12
ACC85278
ID ACC85278 standard; DNA; 2782 BP.

XX ACC85278;
AC
XX 18-SEP-2003 (first entry)
DT
XX Arabidopsis cytokinin oxidase-like protein 4 gene.
DE
XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ds.
KW Arabidopsis thaliana.
OS
XX Arabidopsis thaliana.
XX
PN WO2003050287-A2.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmulling T, Werner T;
XX
DR WPI; 2003-541577/51.
DR P-PSDB; ABR63571.
XX
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 2; Page 153-154; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level of
CC geotropism, cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 2782 BP; 826 A; 538 C; 507 G; 911 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.89e-153 Length: 2782
Score: 1539.50 Matches: 344
Percent Similarity: 44.89% Conservative: 69
Best Local Similarity: 37.39% Mismatches: 80
Query Match: 59.30% Indels: 429
DB: Gaps: 9
US-10-014-101-4 (1-501) x ACC85278 (1-2782)
QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
Db 25 CTCATCACCTTAATAACGCTTTTATAAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84
QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
Db 85 GGCATTGATGTTTCTTACCCATATCACTCAACCTTACGGTCTCAACCGATCCCTTCTCC 144
QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61
Db 145 ATCTCTGCCGCTTCTCACGACTTCGGTAAACATAACCGAAGAAATCCCGCGCGCTCCTC 204

Db 2363 TCTGGTGTACTCTCTTCTATCCCAAAACCGAAACAAGTAAATATTACTTTTGTGATTT 2422
QY 405 ----- 405
Db 2423 TGTTTTATTGAAAGTATATCCCAATAATGTATGTTAAATTTGTTAAACAAGAAATTTATTTT 2482
QY 406 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIle 422
Db 2483 ATTAATAGATGGAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTT 2536
QY 423 TyrIleIleGlyLeuGlnSerAla---ThrProLysAspLeuProGluValGluSer 441
Db 2537 TATGTGATCGGATTACTGCAATCAGTGTGGTCTCAAAATTTGGCAAGAACTTGAAAT 2596
QY 442 ValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeu 461
Db 2597 CTCACACGACAGGTTATTTCAGTTTGTGAAAACTCGGGAATTAAGATTAAAGGAATATTG 2656
QY 462 MetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPhe 481
Db 2657 ATGCACATATACAGAAAGAAAGATTTGGGTAAACATTTTGGACCAAAATGGGATGATTT 2716
QY 482 SerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 2717 TTAAGAAAGAAATATTATGTTTGTATCCCAAAAGACTATTGTCTCCAGGACAAGACATATTT 2776
RESULT 13
ABK28626
ID ABK28626 standard; cDNA; 1572 BP.
XX
AC ABK28626;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX3.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarpy; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmulling T, Werner T;
PI
DR WPI; 2002-130736/17.
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 3; Page 147; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root

CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarpy; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.41e-127 Length: 1572
Score: 1292.00 Matches: 251
Percent Similarity: 59.05% Conservative: 106
Best Local Similarity: 48.55% Mismatches: 138
Query Match: 49.77% Indels: 22
DB: 6 Gaps: 6

US-10-014-101-4 (1-501) x ABK28626 (1-1572)
QY 3 AsnLeuArgLeuMetIleThrLeuIleThr-----ValleuMetIleThrLysSer 19
Db 13 AATCTTCGTTCAAGATTCTGCTTATAGCAATAACAATAGTAATCATCATCTCTCTCA 72
QY 20 SerAsnGlyIleLysIleAspLeuProLysSerLeuAsnLeu----- 33
Db 73 ACTCCGATCACAAACACACATCACCAACCAACCATGGAATATCCTTTACACAACGAATTC 132
QY 34 -----ThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsn 51
Db 133 GCCGGAACAACTCCTCCTCCTCCTCGTGAATCAGCCGCCACAGATTTCGGCCAC 192
QY 52 IleThrThrValThrProGlyValIleCysProSerSerThrAlaAspIleSerArg 71
Db 193 GTCACCAAAATCTCCCTTCGCGCTCTTAATCCCTTCTCCGTTGAAGACATCACAGAT 252
QY 72 LeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db 253 CTCATAAAACTCTCTTTGACTCTCAACTGCTCTTTCTTTAGCCGCTCGTGGTCACGA 312
QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyValIleValAsnMetThrCysIle 111
Db 313 CACAGCCACCGTGGCCAAAGCCTCGGCTAAAGACGGAGTTGTGTCAACATCGGTCATG 372
QY 112 ThrAsp-----ValValValSerLysAspLysLysTyrAlaAspValAlaAla 127
Db 373 GTAAACCGGATCGAGCTATCAAGGTGTCAGACCTGTTTATATGTTGACGTGGACGT 432
QY 128 GlyThrLeuTyrValAspValLeuLysLysThrAlaGluLysGlyValSerProValSer 147
Db 433 GCGTGGCTATGGATTGAGGTGTTGAATAAACTTTGGAGTTAGGGTTAACGCCGTTTCT 492
QY 148 TrpThrAspTyrLeuHisIleThrValGlyThrLeuSerAsnGlyGlyIleGlyGly 167
Db 493 TGGACGGATTATTGTTATTAACAGTCGGTGGACGTTATCAACCGCGGAATTAGTGA 552
QY 168 GlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly 187
Db 553 CAAACGTTTCGGTACGGTCCACAGATCACTAATGTTCTAGAGATGGATGTTATTACTGA 612
QY 188 LysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeu 207
Db 613 AAAGGAGAGATTGCAACTGTTTCCAAAGGACATGAACCTCGGATCTTTCTTCGCGGTGTTA 672
QY 208 GlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaAlaArgIleValLeuAspHisAlaPro 227
Db 673 GGAGGTTTGGTCAATTCGGCATTATAACAAGAGCCAGAATTAACCTTGAGTAGCTCCG 732
QY 228 LysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGln 247

Db 733 AAAAGGGCCAAAGTGGTTAAGGTTTCTATACATAGATTCTCCGAATTCAAGAGATCAA 792
Qy GluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePhe 267
Db 793 GAACGAGTGATATCGAAAACGGAC-----GGTGTAGATTCTTAGAAGGTCCATTATG 846
Qy 268 LeuSerAsnGlyValValAsp-----ThrSerPhePheProProSerAspGlnSer 284
Db 847 GTGGACCATGGCCCGGATAACTGGAGATCCACGTATTATCCACCGTCGATCATTG 906
Qy 285 LysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyr 304
Db 907 AGGATCGCCTCAATGGTCAACACGACATCGTGTCACTACTGCCCTTGAAGTCGTCAAGTAT 966
Qy 305 TyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeu 324
Db 967 TAGCAGCAAACTTCTCAATACACAGTCAACGAGCAATGGAGGAGTTAAGCGATAGTTTA 1026
Qy 325 SerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArg 344
Db 1027 AACCATGTAAGAGGGTTTATGTACGAGAAAGATGTACGTATATGGATTTCCTAAACCGA 1086
Qy 345 ValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeuProHisProTyrP 364
Db 1087 GTTCGAACCGGAGAGCTAAACCTGAATCCAAAGGCAATGGGATGTTCCACATCCATGG 1146
Qy 365 LeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAsp 384
Db 1147 CTTAATCTCTTCGTACCAAAAACCTCAAATCTCCAAATTTGATGGTGTGTTTAAAGGGT 1206
Qy 385 IleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsn 404
Db 1207 ATTATCCTTAAGAAATAACATCACTAGCGGTCTGTCTTGTATTATCCTATGAATCGCAAC 1266
Qy 405 LysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIle 424
Db 1267 AAGTGAATGATCGGATGCTGCTCCGCTATACCCGAG-----GAAGATGTATTTATGCG 1320
Qy 425 IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1321 GTAGGGTTTTTAAGATCCGGGGTTTTTGACAATTTGGAGGCTTTTGTATCAAGAAAAACATG 1380
Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db 1381 GAAATACTGAAGTTTTGTGAGATGCTAATATGGGGTTATACAATATCTTCTCTATCAT 1440
Qy 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484
Db 1441 TCATCACAAGAAGGATGGGTAGACATTTTGGTCCGAGGTGGAATATTTTTCGTAGAGAGA 1500
Qy 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1501 AAATATAAATATGATCCCAAAATGATATTATCACC GGACAAATATATTT 1551

RESULT 14
ACC85295

ID ACC85295 standard; cDNA; 1572 BP.

XX

AC

XX

DT 18-SEP-2003 (first entry)

XX

DE

XX Arabidopsis cytokinin oxidase-like protein 3 cDNA.

KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;

KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.

OS Arabidopsis thaliana.

XX

PN WO2003050287-A2.

XX

PD 19-JUN-2003.

XX 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
XX Schmullling T, Werner T;
PI
XX
DR WPI; 2003-541577/51.
XX
XX Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 3; Page 168-169; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX
SQ Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.41e-127 Length: 1572
Score: 1292.00 Matches: 251
Percent Similarity: 69.05% Conservative: 106
Best Local Similarity: 48.55% Mismatches: 138
Query Match: 49.77% Indels: 22
DB: 8 Gaps: 6

US-10-014-101-4 (1-501) x ACC85295 (1-1572)

Qy 3 AsnLeuArgLeuMetIleThrLeuIleThr-----ValLeuMetIleThrLysSer 19
Db 13 AATCTTCGTTCAACAAGTTCGTCCTTATAGCAATAACAATAGTAAATCATCTCTCTCA 72
Qy 20 SerAsnGlyIleLysIleAspLeuProLysSerLeuAsnLeu----- 33
Db 73 ACTCCGATCACAAACCAACACATCACCAACCATGGAATATCTTTTACACAACGAATTC 132
Qy 34 -----ThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsn 51
Db 133 GCCGGAATACTCACCCTCCTCCTCCTCCGTCGATCAGCCGCCACAGATTTCGGCCAC 192
Qy 52 IleThrThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSerArg 71
Db 193 GTCACCAAAATCTTCCCTTCCCGCGTCTTAATCCCTTCTCCGTTGAAGACATCACAGAT 252
Qy 72 LeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db 253 CTCATAAAACTCTCTTTTGACTCTCAACTGTCTTTTCTCTTAGCCGCTCGTGGTACGGA 312
Qy 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
Db 313 CACAGCCACCGTGGCCAAAGCCTCGGCTAAAGACGGAGTTGTGGTCAACATGCGGTCCATG 372
Qy 112 ThrAsp-----ValValValSerLysAspLysTyrAlaAspValAlaAla 127
Db 373 GTAAACCGGGATCGAGGTATCAAGGTGTCTAGGACCTGTTATATGTTGACGTGGACGCT 432

Qy	128	GlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerProValSer	147
Db	433	GC GTGGCTATGATTTGAGGTGTTGAATAAACTTTGGAGTTAGGGTTAAACGCCGGTTTCT	492
Qy	148	TrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGly	167
Db	493	TGACCGGATTATTGTATTAAACAGTCGGTGGGACGTTATCAAACGGCGGAATTAGTGGA	552
Qy	168	GlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly	187
Db	553	CAAACGTTTCGGTACGGTCCACAGATCACATAATGTTCTAGAGATGGATGTTATTACTGA	612
Qy	188	LysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeu	207
Db	613	AAAGGAGAGATTGCAACTTGTTC AAGGACATGAAC TCGGATCTTTCTTCGCGGTGTTA	672
Qy	208	GlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaPro	227
Db	673	GGAGGTTTGGGTCAATTGGCATTATAACAAGAGCCAGAATTAAAC TTGAAGTAGCTCCG	732
Qy	228	LysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGln	247
Db	733	AAAAGGGCCAAAGTGGTTAAGGTTTCTATACATAGATTCTCCGAATTCAACAGAGATCAA	792
Qy	248	GluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePhe	267
Db	793	GAACGAGTGATATCGAAAACGGAC-----GGTGTAGATTCTTTAGAGGTTCCATTATG	846
Qy	268	LeuSerAsnGlyValValAsp-----ThrSerPhePheProProSerAspGlnSer	284
Db	847	GTGGACCATGGCCACCGGATAACTGGAGATCCACGTATTATCCACC GTCCGATCACTTG	906
Qy	285	LysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyr	304
Db	907	AGGATCGCCTCAATGGTCAAACGACATCGTGTATCTACTGCTTGAAGTCGTCAAGTAT	966
Qy	305	TyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeu	324
Db	967	TACGACGAAACTTCTCAATACACAGTCAACGAGGAAATGGAGAGTTTAAGCGATAGTTTA	1026
Qy	325	SerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArg	344
Db	1027	AACCATGTAAGAGGTTTATGTACGAGAAAGATGTGACGTATATGGATTTCCTAAACCGA	1086
Qy	345	ValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTyr	364
Db	1087	GTTCGAACCGGAGAGCTAAACCTGAAATCCAAAGGCCAAATGGATGTTCCACATCCATGG	1146
Qy	365	LeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAsp	384
Db	1147	CTTAATCTCTTCGTACCAAAAACTCAAATCTCCAATTTGATGATGGTGTGTTTAAAGGT	1206
Qy	385	IleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsn	404
Db	1207	ATTATCCTAAGAAATAACATCACTAGCGGTCTCTGTTCTGTTTATCCTATGATCGCAAC	1266
Qy	405	LysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIle	424
Db	1267	AAGTGAATGATCGGATGTCTGCCGCTATACCCGAG-----GAAGATGTTATTTATGCG	1320
Qy	425	IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu	444
Db	1321	GTAGGGTTTTTAAGATCCCGGGTTTTTGACAAATTTGGGAGGCTTTTGATCAAGAAAAACATG	1380
Qy	445	LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr	464
Db	1381	GAAATACCTGAAGTTTTGTGAGGATGCTAATATGGGGTTATACAATATCTTCTTATCAT	1440
Qy	465	ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg	484
Db	1441	TCATCAACAAGAGGATGGGTAGACATTTTGGTCCGAGGTGGAATATTTTTCGTAGAGAGA	1500
Qy	485	LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe	501

```

Db      1501  AAATATAAATATGATCCCAAAATGATATTATCATCCGGGACAAATATATTT 1551
      |||  ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
RESULT 15
ABK28628
ID  ABK28628 standard; cDNA; 1611 BP.
XX
AC  ABK28628;
XX
DT  09-APR-2002 (first entry)
XX
DE  cDNA encoding A. thaliana cytokinin oxidase AtCKX5.
XX
KW  Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW  root growth; lateral root; adventitious root; root geotropism; he
KW  root meristem; shoot meristem; leaf senescence; parthenocarp; ge
XX
OS  Arabidopsis thaliana.
XX
PN  WO200196580-A2.
XX
PD  20-DEC-2001.
XX
PF  18-JUN-2001; 2001WO-EP006833.
XX
PR  16-JUN-2000; 2000EP-00870132.
PR  27-DEC-2000; 2000US-0258415P.
PR  16-MAR-2001; 2001EP-00870053.
XX
(SCHM/) SCHMULLING T.
(WERN/) WERNER T.
XX
PI  Schmulling T, Werner T;
XX
WPI; 2002-130736/17.
XX
Polynucleotide encoding novel plant protein having cytokinin oxid
activity and the protein useful for stimulating root growth, enhan
the formation of lateral or adventitious roots, altering root geoc
Claim 3; Page 148-149; 154pp; English.
XX
The invention relates to an isolated polynucleotide (I) encoding
plant protein (II) having cytokinin oxidase activity. (I) is usefu
production of transgenic plants, plant cells or tissues; for produ
of altered plants, plant cell or tissues; and for effecting the
expression of (II) where (I) is operably linked to one or more cc
sequences. The methods further comprises regenerating a plant fro
plant cell. (I) and (II) are useful for stimulating root growth;
enhancing the formation of lateral or adventitious roots; alterin
geotropism, leading to an increase in yield; and for screening gni
promoting chemical of herbicides. (I) is useful for increasing the
of the root meristem; increasing root size; increasing the size c
shoot meristem; delaying leaf senescence and altering leaf senesc
increasing leaf thickness; reducing or increasing the vessel size
inducing parthenocarp; improving standability of the seedlings;
increasing branching and for improving lodging resistance. Antibio
to (II) is useful for identifying and obtaining proteins interacti
(II) comprising a screening assay, preferably a two-hybrid screen
assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin
coding sequences and PCR primers of the invention
XX
SQ  Sequence 1611 BP; 416 A; 379 C; 409 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.27e-115 Length: 1611
Score: 1184.00 Matches: 233
Percent Similarity: 66.46% Conservative: 84
Best Local Similarity: 48.85% Mismatches: 142
Query Match: 45.61% Indels: 18
DB: 6 Gaps: 7

US-10-014-101-4 (1-501) x ABK28628 (1-1611)

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 05:53:12 ; Search time 5849 Seconds
(without alignments)
3712.577 Million cell updates/sec

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Perfect score: 2596
Sequence: 1 MANRLMITLITVLMITKSS.....SKRKDLDPKLLSPGQDIF 501

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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16: em_fun:*
17: em_in:*
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22: em_ph:*
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25: em_sts:*
26: em_un:*
27: em_vl:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
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34: em_htg_pln:*
35: em_htg_rod:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2596	100.0	1506	6	AX339729 Sequence
2	2596	100.0	1506	6	AX785077 Sequence
3	2596	100.0	1537	8	BT005653 Arabidops
4	2596	100.0	1687	8	BT004107 Arabidops
5	2588	99.7	1506	8	AF303978 Arabidops
6	2226.5	85.8	2991	6	AX339706 Sequence
7	2226.5	85.8	2991	6	AX785054 Sequence
8	2226.5	85.8	92822	8	AC005917 Arabidops
c	1822	70.2	1575	6	AX339731 Sequence
	1822	70.2	1575	6	AX507394 Sequence
10	1822	70.2	1575	6	AX651615 Sequence
11	1822	70.2	1575	6	AX785079 Sequence
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13	1822	70.2	1863	8	AY054460 Arabidops
14	1822	70.2	1863	8	AF303980 Arabidops
15	1820	70.1	1575	8	AX339710 Sequence
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19	1539.5	59.3	200001	8	ATCHRIV71
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26	1184	45.6	1620	6	AX339737 Sequence
27	1184	45.6	1620	6	AX785085 Sequence
28	1178	45.4	1623	8	AF303982 Arabidops
29	1152	44.4	1776	8	ZMY18377
30	1141.5	44.0	1608	6	AX039923 Sequence
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34	1108.5	42.7	131183	2	AP004181 Oryza sat
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37	1091	42.0	1566	6	AX654568 Sequence
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39	1076	41.4	1677	6	AX653630 Sequence
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41	1063.5	41.0	1590	6	AX653226 Sequence
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43	1056.5	40.7	1728	6	AX339728 Sequence
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ALIGNMENTS

RESULT 1

AX339729
LOCUS AX339729 1506 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 26 from Patent WO0196580.
ACCESSION AX339729
VERSION AX339729.1 GI:18135722
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Schmuelling, T. and Werner, T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 0196580-A 26 20-DEC-2001;
Schmuelling, Thomas (DE); Werner, Tomas (DE)
FEATURES
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1. 1506
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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Score: 2596.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-014-101-4 (1-501) x AX339729 (1-1506)
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QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
Db 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACATAACCAACCGTGACCCCGCGCGGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80
Db 181 ATCTGCCCTCTCCACCGCTGATATCTCTGCTCTCTCCATACCGCGCAACGGAAAA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
Db 241 AGTACATTCCCAAGTAGCGGCTCGTGGCCAAAGCCACTCCTTAAACGGCCAAAGCCTCGGTC 300
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QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGlu 140
Db 361 AAGTACGCTGACGTGGCGCGCGGACGTTATGGGTGGATGTGTTAAGAAAGACGGCGGAG 420
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QY 201 GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg 220
Db 601 GAATTGTTCTATGGAGTGTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGA 660
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QY 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260
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QY 261 TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProPro 280
Db 781 TATTTAGAAGGTCAAAATATTTCTATCAAAACGGTGTGCTGTGACACCTCTTTTTCACCT 840
QY 281 SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu 300
Db 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA 900
QY 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320
Db 901 GTAGCCAAAGTATTATGATGATGCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA 960
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340
Db 961 ACGAAAACATTAAGTTACTTGCCTGGGTTTCATATCAATCAATGACGACGCTGCTTCCGAT 1020
QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu 360
Db 1021 TTCTTGAAACCGTGTACATGTGCAAGAAAAATAAACTCAGATCTTTGGGATTATGGGAACCT 1080
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QY 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400
Db 1141 GTTGTCAAAGACATCTCTTAAAGCAAAATCAGCTTCGGGACTCGCTCTCTCTATCCA 1200
QY 401 ThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp 420
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Db 1381 CTAATGCATTATATACTAGTAAAGAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT 1440
QY 481 PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle 500
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QY 501 Phe 501
Db 1501 TTT 1503
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AX785077
LOCUS AX785077 1506 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 26 from Patent WO03050287.
ACCESSION AX785077
VERSION AX785077.1 GI:32952908
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Schumullig,T. and Werner,T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 03050287-A 26 19-JUN-2003;
Schumullig, Thomas (DE) ; Werner, Tomas (DE)

FEATURES

source Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 2.89e-213 Length: 1506
Score: 2596.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-014-101-4 (1-501) x AX785077 (1-1506)

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QY	21	AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer	40
Db	61	AACGGTATTAAATTGATTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC	120
QY	41	IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal	60
Db	121	ATCATCTCCGACGCCCTCTCATGACTTCGGAAACATAACCAACCGTGACCCCGCGCGTA	180
QY	61	IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys	80
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QY	81	SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal	100
Db	241	AGTACATTCCAAGTAGCGGTCGTGGCCAAGGCCACTCTTTAAACGGCCCAAGCCTCGGTC	300
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QY	121	LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGlu	140
Db	361	AAGTACGCTGACGTGGCGCGGACGTTATGGGTGGATGTCTTAAAGACGCGCGGAG	420
QY	141	LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeu	160
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QY	261	TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProPro	280
Db	781	TATTTAGAAGGTCAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTTCCACCT	840
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QY	341	PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu	360
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QY	361	ProHisProTrpLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly	380
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QY	381	ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro	400
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QY	421	ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu	440
Db	1261	GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAG	1320
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QY	461	LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp	480
Db	1381	CTAATGCATTATACTAGTAAAGAGATTGGATTGGATTCAGCATTTTGATCAAAATGGGATGAT	1440
QY	481	PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle	500
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BT005653 1537 bp mRNA linear PLN 15-MAR-2003
LOCUS Arabidopsis thaliana clone U20989 putative cytochrome oxidase
DEFINITION (At2g19500) mRNA, complete cds.
ACCESSION BT005653
VERSION BT005653.1 GI:28973496
KEYWORDS FLI_CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1537)
REFERENCE Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
AUTHORS Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wong,C., Wu,H.C.,
Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,

Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Arabidopsis Open Reading Frame (ORF) Clones Unpublished 2 (bases 1 to 1537)

Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission Submitted (15-MAR-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.

Location/Qualifiers

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3'UTR

ORIGIN

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Pred. No.: 2,97e-213 Length: 1537

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Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

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Db	181	ATCTGCCCTCTCCACCCGCTGATATCTCTCGTCTCTCCAATACGCCGCAACGGAATA	240
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QY	281	SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu	300
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QY	341	PheLeuAsnArgValHisValGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu	360
Db	1021	TTCTTGAACCGTGATCATGTGGAAGAAATAAACTCAGATCTTTGGGATTATGGGAAC	1080
QY	361	ProHisProTrrPleuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly	380
Db	1081	CCTCATCCTTGGCTTAACCTCTACGTTCTCFAAATCTCGGATTCICGATTTTCATAACGGT	1140
QY	381	ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro	400
Db	1141	GTTGTCAAAGACATCTCTTAAAGCAAAATCAGCTTCGGACTCGCTCTTCTCTATCCA	1200
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Db	1201	ACAAACCGGAATAAATGGGACAATCGTATGTCGGCGATGATACCCAGAGATCGATGAAGAT	1260
QY	421	ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu	440
Db	1261	GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAG	1320
QY	441	SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr	460
Db	1321	AGCGTTAACGAGAGATAATTAGTTTTTGCAAGGATTCAGGTATTAAAGTAATAGCAATAT	1380
QY	461	LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp	480
Db	1381	CTAATGCATTATACTAGTAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT	1440
QY	481	PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle	500
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QY	501	Phe 501	
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BT004107			
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DEFINITION	Arabidopsis thaliana clone RAFL15-29-H04 (R20989)	putative	cytokinin oxidase (At2g19500) mRNA, complete cds.
ACCESSION	BT004107	GI:28393415	
VERSION	BT004107.1		
KEYWORDS	FLJ CDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.		
TITLE	Arabidopsis Full Length cDNA Clones		
JOURNAL	Unpublished		
REFERENCE			
AUTHORS	Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-FEB-2003)		
COMMENT	Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		
	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,		

Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.			
The Salk, Stanford, PGEN (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.			
Yamada,K. (SSP/PGEN) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEN) contributed equally to this work as PIs.			
Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.			
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Best Local Similarity:	100.00%	Mismatches:	0
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DB:	8	Gaps:	0
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DEFINITION Arabidopsis thaliana cytokinin oxidase (CKX2) mRNA, complete cds.
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VERSION AF303978.1 GI:11120507
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
REFERENCE 1 (bases 1 to 1506)
AUTHORS Bilyeu,K.D., Laskey,J.G., Riekhof,W.R., VanVickle,S. and Morris,R.O.
TITLE A family of cytokinin oxidases from Arabidopsis thaliana
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1506)
AUTHORS Bilyeu,K.D., Laskey,J.G., Riekhof,W.R., VanVickle,S. and Morris,R.O.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA
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ORGANISM Arabidopsis thaliana
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REFERENCE Schmulling,T. and Werner,T.
AUTHORS Method for modifying plant morphology, biochemistry and physiology
TITLE Patent: WO 0196580-A 3 20-DEC-2001;
JOURNAL Schmulling, Thomas (DE); Werner, Tomas (DE)
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Query Match: 85.77% Indels: 499
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VERSION AX785054.1 GI:32952890
KEYWORDS
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Schmulling,T. and Werner,T.
AUTHORS Method for modifying plant morphology, biochemistry and physiology
TITLE Patent: WO 03050287-A 3 19-JUN-2003;
JOURNAL Schmulling, Thomas (DE) ; Werner, Tomas (DE)
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AC005917/c
LOCUS

AC005917 92822 bp DNA linear PLN 27-FEB-2002

DEFINITION Arabidopsis thaliana chromosome 2 clone F3P11 map CIC06E08, complete sequence.
ACCESSION AC005917
VERSION AC005917.3 GI:20197478
KEYWORDS HTG.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 92822)
Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E., Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.-I., Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D., Nierman,W.C., Fraser,C.M. and Venter,J.C.
Unpublished
2 (bases 1 to 92822)
Lin,X.
Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 92822)
Town,C.D. and Kaul,S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598497.
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Db 40420 CTTTTTGATGTCAATATATAAATCCTTGTATTAGAGTCAAGCTCTTTCAATTAGTCAACT 40361
QY 228 ----- 228
Db 40360 ACTCAAAATATACTCCAAAGTTTAGAATATAGTCTTCTGACTAATTAGAATCTTACAACCG 40301
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Db 40120 TCTCTAAATGAAATTGTAGGCC-AAATGGTTTCGGATGCTCTACAGTGATTTCCACAAC 40062
QY 242 rPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLe 262
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QY 262 uGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAs 282
Db 40001 AGAAGGTCAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTTTTCCACCTTCAGA 39942
QY 282 pGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAl 302
Db 39941 TCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGC 39882
QY 302 aLysTyrTyrAspProAsnLeuProIleIleSerLys----- 315
Db 39881 CAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTACTACACATTACATTTT 39822
QY 315 ----- 315
Db 39821 CATCATCGTTTTTATCATACCATAAGATATTTAAATGATTCATCATTCGCCACACATTAA 39762
QY 315 ----- 315
Db 39761 ATATTTCATCATCATCGTTACATTTTTTTTTTGCACTCTTATGCTTCTCTATAATCTACTA 39702

QY 316 -----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerM 333
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QY 333 etHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuA 353
Db 39641 TGCACGACGTGGCCTACTTCGATTTCTTGAACCGTGTACATGTGGAAGAAATAAACTCA 39582
QY 353 rgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSerA 373
Db 39581 GATCTTTGGGATTATGGAACTTCTCTCATCCTGGCTTAACCTCTACGTTCTCTAAATCTC 39522
QY 373 rgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAlas 393
Db 39521 GGATTTCTCGATTTTTCATAAACGGTGTGTGTCAAAGACATTTCTTTAAGCAAAAAATCAGCTT 39462
QY 393 erGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405
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QY 425 leGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluL 445
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QY 445 ysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrT 465
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QY 465 hrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArgL 485
Db 39162 CTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTTCGAAGAGGA 39103
QY 485 ysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 39102 AAGATCTATTGATCCCAAGAAACTGTTATCTCCGGGCAAGACATCTTT 39053

RESULT 9
AX339731 LOCUS AX339731 1575 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 28 from Patent WO0196580.
ACCESSION AX339731
VERSION AX339731.1 GI:18135724
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Schmulling,T. and Werner,T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 0196580-A 28 20-DEC-2001;
Schmulling, Thomas (DE) ; Werner, Tomas (DE)
FEATURES
source
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"

ORIGIN
Alignment Scores: 8.22e-147 Length: 1575
Pred. No.: 1822.00 Matches: 345
Score: 80.08% Conservative: 69
Percent Similarity:

Best Local Similarity: 66.73%			Mismatches: 79		
Query Match: 70.18%			Indels: 24		
DB: 6			Gaps: 5		
US-10-014-101-4 (1-501) x AX339731 (1-1575)					
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QY	22	GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle	41		
Db	85	GGCATTGATGTTTTCTTACCCATATCACTCAACCTTACGGTCTCTAACCGATCCCTTCTCTC	144		
QY	42	IleSerAlaAlaSerHisAspPheGlyAsnIleThrValThrProGlyGlyValIle	61		
Db	145	ATCTCTGCCGCTTCTCACGACTTCGGTAACATAACCGACGAAATCCCGCGCGCTCTCTC	204		
QY	62	CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly-----	79		
Db	205	TGCCCTTCTCCACACCGAGGTGGCTCGTCTCTCCGTTTCGTTACCGAGGATTTCTCT	264		
QY	80	-----LysSerThrPheGlnValAlaAlaArgGlyGlnGly	91		
Db	265	TACAATAAAGGCTCAACACGCCCGCTCTACTTTCAAAGTGGTGTCTCGAGGCCAAGGC	324		
QY	92	HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle	111		
Db	325	CACCTCCCTCGTGGCCCAAGCCTCTGCACCCGGAGGTGTCTGCTGAACATGACGTGTCTC	384		
QY	112	-----ThrAspValValSerLysAspLysLysTyrAlaAspVal	125		
Db	385	GCCATGGCGGCTAAACACGCGCGGTTGTTATCTCGCAGACGGGACTTACGCTGACGTG	444		
QY	126	AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro	145		
Db	445	GCTGCCGCGACGATGTGGTGGATGTTCTGAAGCGCGGTGGATAGAGCGCTCTCGCCG	504		
QY	146	ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle	165		
Db	505	GTTACATGGACGGATTATTTGTATCTCAGCGTCGGCGGGACGTTGTCTGAACGCTGGAATC	564		
QY	166	GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle	185		
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QY	186	ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly	205		
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Db	745	GCACCCACAAGGGTGAAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA	804		
QY	246	AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGln	265		
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QY	286	ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr	305		
Db	925	GTCGCATCTCTTGTAATGACCAACCGGATCATCTATGTTCTCGAAGTAGCCAAGTATTAT	984		
QY	306	AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer	325		
Db	985	GACAGAACCACCCCTTCCCATTTATTGACCGGTGATTGACACGTTAAGTAGAACTCTAGGT	1044		

QY	326	TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal	345		
Db	1045	TTGCTCCAGGGTTTATGTTGTTACAGATGTTCCGTATTTCGATTTCCTTGAACCGTGT	1104		
QY	346	HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu	365		
Db	1105	CGAAACGAAGAAGATAAACTCAGATCTTTAGGACTATGGGAAGTTCTCTCATCCATGGCTT	1164		
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QY	406	TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle	425		
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QY	426	GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu	444		
Db	1339	GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAAGTTGAAAATCTCAACGAC	1398		
QY	445	LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMethIleTyr	464		
Db	1399	AAGTTATTGAGTTTGTGAAAACCTCGGGAATTAAGATTAAAGAAATATTTTGATGCACTAT	1458		
QY	465	ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg	484		
Db	1459	ACAAGAAAAGAGATTGGGTTAAACATTTTGGACCACAAATGGGATGATTTTTTAAAGAAAG	1518		
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RESULT 10

AX507394 LOCUS AX507394 1575 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 2089 from Patent WO0216655.
ACCESSION AX507394
VERSION AX507394.1 GI:23388631

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing same, and methods of use
JOURNAL Patent: WO 0216655-A 2089 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG (CH)

FEATURES

source Location/Qualifiers
1..1575
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Alignment Scores:
Pred. No.: 8.22e-147 Length: 1575
Score: 1822.00 Matches: 345
Percent Similarity: 80.08% Conservative: 69
Best Local Similarity: 66.73% Mismatches: 79
Query Match: 70.18% Indels: 24
DB: Gaps: 5

US-10-014-101-4 (1-501) x AX507394 (1-1575)

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QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Dbb 265 TACAATAAAGGCTCAACACGCGCGCTCTACTTTCAAGTGGCTGCTCGAGGCCAAGGC 324
QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
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QY 112 -----ThrAspValValValSerLysAspLysLysIleValAlaAspVal 125
Dbb 385 GCCATGGCGGCTAAACACGCGCGGTGTTATCTCGCAGACGGGACTTACGCTGACGTG 444
QY 126 AlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145
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QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
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AX785079 1575 bp DNA linear PAT 17-JUL-2003
LOCUS Sequence 28 from Patent WO03050287.
DEFINITION AX785079
ACCESSION AX785079
VERSION AX785079.1 GI:32952910
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
REFERENCE
AUTHORS Schmulling, T. and Werner, T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 03050287-A 28 19-JUN-2003;
Schmulling, Thomas (DE); Werner, Tomas (DE)
FEATURES
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 8.22e-147 Length: 1575
Score: 1822.00 Matches: 345
Percent Similarity: 80.08% Conservative: 69
Best Local Similarity: 66.73% Mismatches: 79
Query Match: 70.18% Indels: 24
DB: 6 Gaps: 5
US-10-014-101-4 (1-501) x AX785079 (1-1575)
QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
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QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
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QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
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QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
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 Db 1399 AAGGTTATTACGTTTGTGAAAACTCGGAATTAAGATTAAAGGAATATTGATGCACCTAT 1458
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RESULT 13
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 DEFINITION mRNA, complete cds.
 ACCESSION BT000179
 VERSION BT000179.1 GI:23197941
 KEYWORDS FLI_CDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1655)
 REFERENCE Nguyen,M., Karlin-Neumann,G., Southwick,A., Tripp,M., Miranda,M.,
 Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
 Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
 Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
 Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
 Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
 Direct Submission
 Submitted (19-SEP-2002) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT e-mail for correspondence: arab@sequence.stanford.edu
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
 Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.
 The Salk, Stanford, PGEC (SSP) Consortium members constructed and
 sequenced the pENTR (ORF) clones using the RAFL cDNAs: Nguyen,M.,
 Southwick,A., Tripp,M., Palm,C.J., Jones,T., Wu,T., Chen,H.,
 Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
 Lee,J.M., Kim,C.J., Quach,H.L., Shinn,P., Tang,C.C., Toroumi,M.,
 Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S.,
 Ecker,J., Theologis,A. and Davis,R.W.
 Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
 equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
 (SSP/Stanford) contributed equally to this work as PIs.
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ORIGIN

Alignment Scores:
Pred. No.: 8.81e-147 Length: 1655
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Percent Similarity: 80.08% Conservative: 69
Best Local Similarity: 66.73% Mismatches: 79
Query Match: 70.18% Indels: 24
DB: 8 Gaps: 5

US-10-014-101-4 (1-501) x BT000179 (1-1655)

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RESULT 14

AY054460

LOCUS

DEFINITION

Arabidopsis thaliana cytochrome oxidase-like protein (At4g29740;

AY054460.1 GI:15450760

VERSION

FLI_CDNA.

SOURCE

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1863)

1863 bp mRNA linear PLN 05-SEP-2001
Arabidopsis thaliana cytochrome oxidase-like protein (At4g29740;
T16L4.250) mRNA, complete cds.

AUTHORS Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Palm,C.J., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES
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ORIGIN

Alignment Scores:
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Score: 1822.00 Matches: 345
Percent Similarity: 80.08% Conservative: 69
Best Local Similarity: 66.73% Mismatches: 79
Query Match: 70.18% Indels: 24
DB: 8 Gaps: 5

US-10-014-101-4 (1-501) x AY054460 (1-1863)

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GenCore version 5.1.6
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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	23	519	20.0	741	14	CF210007 CAB20005
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38	493	19.0	488	10	AW429072	AW429072 EST306444
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41	489	18.8	802	29	CG451590	CG451590 OGVGM89TH
42	485	18.7	750	29	CG322138	CG322138 OGXC022TH
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ALIGNMENTS

RESULT 1	AY112108	AY112108	1776 bp	mRNA	linear	HTC 17-OCT-2002
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SOURCE	Zea mays					
ORGANISM	Zea mays					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD					
	clade; Panicoideae; Andropogoneae; Zea.					
REFERENCE	1	(bases 1 to 1776)				

AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1776)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.

FEATURES Location/Qualifiers
1..1776
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:630384"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

Alignment Scores:
Pred. No.: 2.59e-96 Length: 1776
Score: 893.00 Matches: 199
Percent Similarity: 54.18% Conservative: 67
Best Local Similarity: 40.53% Mismatches: 197
Query Match: 34.40% Indels: 28
DB: 11 Gaps: 11

US-10-014-101-4 (1-501) x AY112108 (1-1776)

QY 35 LeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThr 54
Db 176 CTCCGGACCGACAGCAACGCGACGGCGGCGCTCGACGGACTTCGGCAACATCNCNNNN 235
QY 55 ValThrProGlyValIleCysProSerThrAlaAspIleSerArgLeuLeuGln 74
Db 236 NNN 295
QY 75 TyrAlaAlaAsnGlyLysSer-----ThrPheGlnValAlaAlaArgGlyGlnGlyHis 92
Db 296 ---GCGGCAACTCCACCCCGGGTGGCCCTACACCATCGCGTTCGCGCGCGCGGCAC 352
QY 93 SerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIleThr 112
Db 353 TCCCTCATGGCCAGNN 412
QY 113 AspValVal-----ValSerLysAspLysLysTyrAlaAspValAla 126
Db 413 NNN 472
QY 127 AlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerProVal 146
Db 473 GCGGAGCAGGTGTGGATCGACGTCGTCGCGCGCTCNCNNNNNNNNNNNNNNNNNNNN 532
QY 147 SerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGly 166
Db 533 NNNNGACCGACTACCTCTACCTACCGTCGCGGCACCGTGTCCACGACGAGCATCAGC 592
QY 167 GlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThr 186

Db 593 GGCCAGGGGTTCCGCCACGGCCACAGATATCTAACGTGCTGGAGATGGACGTTATCACC 652
QY 187 GlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyVal 206
Db 653 GGCCATGGGAGATGGTGACGTGCTCCACGACGCTGAACGCGGACCTGTTCCGANNNNNN 712
QY 207 LeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAla 226
Db 713 NNN 772
QY 227 ProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAsp 246
Db 773 NNN 832
QY 247 GlnGluArgLeuIleSerMetAlaAsnAspIleGly-----ValAsp 260
Db 833 CAGGAGCGGCNN 892
QY 261 TyrLeuGluGlyGlnIlePhe-----LeuSerAsnGlyValValAspThrSer 276
Db 893 TACGTGGAAGGGTCCGTGTTCTGTGAACACAGAGCCTGGCAGCCTGGCGAACACGGGG 952
QY 277 PhePheProProSerAspGlnSerLysValAlaAspLeuValLysGlnHisGly----- 294
Db 953 TTCTTCACCGACGCGACGTCGCCGGATCGTCGGCTCGCGGGGACGGGAACGCCACC 1012
QY 295 IleIleTyrValLeuGluValAlaLysTyrTyrAsp-----AspProAsnLeuProIle 312
Db 1013 ACCGTGTACAGCATCGAGGCCACGCTCAACTACGACNNNNNNNNNNNNNNNNNNNNNN 1072
QY 313 IleSerLysValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSer 332
Db 1073 NNNNNCCAGGAGCTCGGTCGTCGTCGGCACGCTAGCTACGTGGAGGGTTCGCGTTC 1132
QY 333 MetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeu 352
Db 1133 CAGCGCGACGTGGCTACCGCGCGGTTCCTTGACCGGGTGACCGCGGAGGAGTGGCGCTC 1192
QY 353 ArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSer 372
Db 1193 AACAAAGCTGGGGTGTGGGGGTGCCGACCCCGTGGCTCAACATGTTCTGTCGCGGCTCG 1252
QY 373 ArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAla 392
Db 1253 CGCATCGCCGACTTCGACCGCGCGGTGTTCAGGGGCATC---CTGACGGGCACCGACATC 1309
QY 393 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 412
Db 1310 GTCGCGCCGCTCATCGTCTANNNNNTCAACAAATCCATGTGGACGACGCGCATGTGGCG 1369
QY 413 MetIleProGluIleAspGluAspValIleTyrIleIleGlyLeuLeu---GlnSerAla 431
Db 1370 GCGACCGCG-----TCTGAGGACGTGTTCTACCGGTGTCGCTGCTCTCTCTCGTCGGTG 1423
QY 432 ThrProLysAspLeuProGluValGluSerValAsnGluLysIleIleArgPheCysLys 451
Db 1424 GCGCCCAACGACCTGGCGAGGCTGCAGGAGCAGAGACAGGAGGATCCTGCGCTTCTGCGAC 1483
QY 452 AspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSerLysGluAspTrpIle 471
Db 1484 CTCGCGCGGATCCAGTACAAGACCTACCTGGCGCGGCACACGACCGCAGTGTGGTTC 1543
QY 472 GluHisPheGly---SerLysTrpAspPheSerLysArgLysAspLeuPheAspPro 490
Db 1544 CGCCACTTCGGCGCGCCCAAGTGAATCGTTCGTGGAGATGAAGACAAGTACGACCCC 1603
QY 491 LysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1604 AAGAGGCTGCTCTNNNNNGGCCAGGACATCTTC 1636

RESULT 2
AU236872
LOCUS AU236872 561 bp mRNA linear EST 01-APR-2002

DEFINITION AU236872 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-29-H04 5', mRNA sequence.

ACCESSION AU236872

VERSION AU236872.1 GI:19876041

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 561)

REFERENCE Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.

AUTHORS Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002)

TITLE Contact: Motoaki Seki

JOURNAL Plant Functional Genomics Research Group

COMMENT RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda Pfu-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sali. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source

1. .561

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="RAFL15-29-H04"

/tissue_type="mixture of silique and flower"

/lab_host="DH10B"

/clone_lib="RAFL15"

/note="Site_1: BamHI; Site_2: Sali"

ORIGIN

Alignment Scores:

Pred. No.: 6.94e-87 Length: 561

Score: 808.00 Matches: 166

Percent Similarity: 97.65% Conservative: 0

Best Local Similarity: 97.65% Mismatches: 2

Query Match: 31.12% Indels: 2

DB: 9 Gaps: 0

US-10-014-101-4 (1-501) x AU236872 (1-561)

QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20

DB 55 ATGGCTAATCTCGTTTAATGATCACCTTAATCACGGTTTTAATGATCACCAATCATCA 114

QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40

DB 115 AACGGTATTAAATTGATTACCTAAATCCCTTAACCTCACCCCTCTTACCGATCCTTCC 174

QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60

DB 175 ATCATCTCCGCAGCCTCTCATGACTTCGGAAACATAACCAACCGTGACCCCGCGCGTA 234

QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80

DB 235 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCCTCCAATACGCGCAACGAAAA 294

QY 81 SerThrPheGlnValAlaAlaAargGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100

DB 295 AGTACATTCCAAAGTAGGGCTCGTGGCCCAAGGCCACTCTTTAAACGSCCAAGCCTCGGC 354

QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValSerLysAspLys 120

DB 355 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAAGACAAG 414

QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrpValAspValLeuLysLysThrAlaGlu 140

DB 415 AAGTACGCTGACGTGGCGCGGACGCTTATGGTGGATGTGCTTAAGAAGACGCGGAG 474

QY 141 LysGlyValSerProValSerThrAspTyrLeuHisIleThr-ValGlyGlyThrIle 160

DB 475 AAAGGGGTGTCGCCGGTTTCTTGACGGATTATTTGCATATAACCCGTCGGANGAACGTT 534

QY 160 uSerAsnGlyGly-IleGlyGlyGln 168

DB 535 NTCNAATGGTGAATTTGGTGGTCAA 560

RESULT 3

BH575041/c

LOCUS BH575041 838 bp DNA linear GSS 14-DEC-2001

DEFINITION BOG82TR BOGB Brassica oleracea genomic clone BOG82, genomic survey sequence.

ACCESSION BH575041

VERSION BH575041.1 GI:17827114

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 838)

REFERENCE Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

AUTHORS Whole genome shotgun sequencing of Brassica oleracea

TITLE Unpublished (2001)

JOURNAL Other_GSSs: BOG82TF

COMMENT Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

FEATURES

Location/Qualifiers

1. .838

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOG82"

/clone_lib="BOGB"

/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Alignment Scores:

Pred. No.: 6.56e-84 Length: 838

Score: 786.00 Matches: 154

Percent Similarity: 79.62% Conservative: 14

Best Local Similarity: 72.99% Mismatches: 16

Query Match: 30.28% Indels: 28

DB: 2 Gaps: 2

US-10-014-101-4 (1-501) x BH575041 (1-838)

QY 316 ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAsp 335

DB 638 GTGATTGACAAAGTTAACTAAACCCCTAAGTACCTGCCCGGTTTATATCAATGCACGAC 579

QY 336 ValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeu 355

DB 578 GTGCTCTACTTTGATTTCCTGAACCGGTGACAAGTTGAAGAAGATAAACTCAGATCTCTG 519

Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location/Qualifiers
1..688
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea Tol000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN

Alignment Scores:
Pred. No.: 2.05e-72 Length: 688
Score: 690.00 Matches: 132
Percent Similarity: 88.82% Conservative: 11
Best Local Similarity: 81.99% Mismatches: 18
Query Match: 26.58% Indels: 0
DB: 28 Gaps: 0

US-10-014-101-4 (1-501) x BZ006516 (1-688)

Qy	27	LeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIleIleSerAlaAlaSer	46
Db	30	CTACCCAAATCGTTAAACCTCACCCCTCCTAAACCGATCCTTCGCCCATCTCCGCCCTCT	89
Qy	47	HisAspPheGlyAsnIleThrThrValThrProGlyGlyValIleCysProSerSerThr	66
Db	90	CACGATTTTGGAAACATCACTACCGTGATACCCGGTGCGGTGATCTGCCCTTCCTCTCCC	149
Qy	67	AlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAla	86
Db	150	GCTGAGATATCCCGTCTCCTCAGCTACGCTCTAACGGAGAAAGAAAGTTCCAAGTGGCA	209
Qy	87	AlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleVal	106
Db	210	GCTCGCGGCCAAGCCACATCCTTGAAGGCTCAAGCAGCAGTCCTCAACGGAGTAAATCGTC	269
Qy	107	AsnMetThrCysIleThrAspValValSerLysAspLysLysTyrAlaAspValAla	126
Db	270	AACATGACGTGTTCGTCGTCGTAGTGATTTCAGATGACATGAAGTATGCTGACGTGGCC	329
Qy	127	AlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerProVal	146
Db	330	GGTGGGACGTTATGGGTTGATGTCTGAAAAATACGGCGGAGAAAGCGTTTCGCCGTT	389
Qy	147	SerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGly	166
Db	390	TCTTGGACGGATTATTTCATGTTAGCATCGAGGAACACTGTCAATGCTGGAATCGGC	449
Qy	167	GlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThr	186
Db	450	GCTGAAGTGTTTAGAAACGGTCCTCAGATTAGTAACGTCCTTGAGTTGGACGTTATAACT	509
Qy	187	Gly 187	
Db	510	GGT 512	

RESULT 6
CF439478
LOCUS
DEFINITION EST675823 normalized cDNA library of onion Allium cepa clone
ACCESSION ACAAS20, mRNA sequence.
VERSION CF439478
KEYWORDS CF439478.1 GI:34462168
SOURCE Allium cepa (onion)


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DB: 28 Gaps: 2
US-10-014-101-4 (1-501) x BZ078445 (1-792)
QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMet----- 15
Db ATGGCTGATCTTCTCTAATGATAACTCTAATGACGGTTCTGATTTATTTACTTCCAAGC 436
QY 16 IleThrLysSerSerAsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeu 35
Db TGTATCAAATCGTCA-----GAGATTATTCTACCCAAATCGTTAAACCTCACCTC 385
QY 36 SerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsnIleThrVal 55
Db CTAACCGATCCTTCGCGCATCTCCGCGCCTCTCACGATTGTGAAACATCACTACCGTG 325
QY 56 ThrProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyr 75
Db ATACCCGTTGGCGTGATCTGCCCTTCTCTCCGCTGAGATATCCCGTCTCTCCTCAGTAC 265
QY 76 AlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsn 95
Db GCCTCTAACGGAGAGAAAGTTCCAAGTGGCAGCTCGCGGCAAGGCCACTCCTTGAAG 205
QY 96 GlyGlnAlaSerValSerGlyGlyValIleValAlaAsnMetThrCysIleThrAspValVal 115
Db GGTCGAAGCAGCAGTCCTCAACGGAGTAATCGTCAACATGACGTGTCTCGCTGGCGTAGTG 145
QY 116 ValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeu 135
Db ATTTTCAGATGACATGAAGTATGCTGACGTGGCGCGTGGGACGTATGGGTTGATGTGCTG 85
QY 136 LysLysThrAlaGluLysGlyValSerProValSerTyrThrAspTyrLeuHisIleThr 155
Db AAAAATACGGCGGAGAAAGCGGTTTCGCGGTTTCTTGGACGGATTATTTCATGTAGTA 25
QY 156 Val 156
Db ATT 22

RESULT 10
CG289653
LOCUS CG289653 969 bp DNA linear GSS 25-AUG-2003
DEFINITION OGWFN30TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBma0566F12,
genomic survey sequence.
ACCESSION CG289653
VERSION CG289653.1 GI:34203867
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 969)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGWFN30TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
LOCATION/Qualifiers
source 1..969
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/db_xref="taxon:4577"
/clone="ZMMBma0566F12"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 3.58e-59 Length: 969
Score: 583.00 Matches: 132
Percent Similarity: 54.63% Conservative: 45
Best Local Similarity: 40.74% Mismatches: 70
Query Match: 22.46% Indels: 78
DB: 29 Gaps: 7

US-10-014-101-4 (1-501) x CG289653 (1-969)
QY 173 GlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly-Lys----- 188
Db 2 GGTCCGCAGATCGCCAACGTCGTCGAACTCGATGTCGTGCACAGGTATCGATCGATCGATG 61
QY 188 ----- 188
Db 62 GTTACACTCCCTGTGATAATTACATAAGCAGCTAATCACACACCAATGCTAATAATAGTT 121
QY 189 -----GlyGluMetLeuThrCysSerArgGlnLeuAs 199
Db 122 TATACATGTGATGAACAATGCAGGCACAGGTGAGATGGTGACATGCTCCATGGACGTGA 181
QY 199 nProGluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAl 219
Db 182 CTCGGACCTGTTTCATGGCAGCTCTAGCGGGTTAGGCCAATTTCGGGGTCTATAACCA 241
QY 219 aArgIleValLeuAspHisAlaProLysArgAlaLysTyrPheArgMetLeuTyrSerAs 239
Db 242 ACGGATCCGGCTTGAGCCGGCGCCCAAGAGGGTGCCTGGGTTCGACTTGCCTACACCG 301
QY 239 pPheThrThrPheThrLysAspGlnGluArgLeuIleSer---MetAlaAsnAspIleG 258
Db 302 CGTCGCTACTTTCACCAAGGATCAGGAGTTTCTCATATCGAACCGGACTAGCCAAGTC 361
QY 258 yValAspTyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAsp----- 274
Db 362 GTTCGACTACGTCGAAGGCCAGGTCCAGCTCAACCGGTCTTGGTTCGAAGGTCCCAAATC 421
QY 275 -ThrSerPhePheProProSerAspGlnSerLysValAlaAspLeuValLysGlnHisG 294
Db 422 AACACCCCTTCTTCTCCGGCGCCGATCTTGCTAGACTTGCTGGACTCGCGTCGAGGACC 481
QY 294 y-----IleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsnLeuProI 312
Db 482 ACCTACTGCAATATACTACATCGAAGGCCCATGTACTACACCGAGACACCGCCATATC 541
QY 312 eIleSerLysVal-----IleAspThrLeuThrLysThr----- 323
Db 542 TGTGGACAAGGTACAGATCAGCTTCGAGCCAGGGTTTCCTCGTTCCACCAAGGACGTGAC 601
QY 323 ----- 323
Db 602 TCAATGCTTTGGACAAAAGGAAACTCATTCGTTGTTGCTATATGAATCGTTGCAGAAAAT 661
QY 324 -----LeuSerTyrLeuProGlyPheIleSerMetHisAspValAl 337
Db 662 GAAGGCACCTCTGGATCAGCTGAGCTTCGAGCCAGGGTTTCCTCGTTCCACCAAGGACGTG 721
QY 337 aTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLe 357
Db 722 GTTCGTGCAGTTCCTCGACCGGGTGCAGGAGGAGAGGGTGTCTCGGTTCAGCCGCGCG 781
QY 357 uTrpGluLeuProHisProTyrLeuAsnLeuTyrValProLysSerArgIleLeuAspPh 377
Db 782 GTGGGAGGTACCAACCCCATGGCTGAATCTCTTCGTCGCCGGTTCGGGCATCCTCGACTT 841
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Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..948
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0599p16"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

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Alignment Scores:	
Pred. No.:	
Score:	1.6e-56
Percent Similarity:	561.00
Best Local Similarity:	52.87%
Best Local Similarity:	42.04%
Query Match:	21.61%
DB.	29
	29
	Gap:
	Indels:
	Mismatches:
	Conservative:
	Matches:
	Length:
	948
	132
	34
	81
	68
	6

US-10-014-101-4 (1-501) x CG460090 (1-948)

Qy 35 LeuSerThrAspProSerIleSerAlaAlaSerHisAspPheGlyAsnIleThrThr 54

DB	946	ATCAGCAGGAGCAGCGCAACCATCAAGGCATCCATGGACTTTGGCCACATTGTGAGA	887
QY	55	ValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGln	74

886	GCTATCCCAAGCGGGGTATTCCATCCGACCTCACCCAGCGACATTGCCGCCCTAATCCGG	D b
75	TyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeu	Q y
826	CTCTCACTCTCCCAAGCCCAAGCCCTTCGAGTGGCGCCACGCGGCGGAGGCCACTCCGCT	D b
95	AsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIleThrAspVal	Q y

db 766 CGAGGCGAGGCCCTCGCGGTGGCGGGGTGCTCGACATCGGCTCGTCCACGAC---

```

QY      115 ValValSerLysAspLysLys----- 121
      |||
Db      709 ---CACGACCACGACCACCGTGTGTCATGTCGTCACCGCATGAATAATGCAGTCCCA 653
QY      122 -----ThrAlaSerValAlaAlaClyVThrLeuTrovAlAspValLeuIlyLysVstHraAla 139

```

QY	122	-----IYAAASPVALAIAALAGLYIMLENIIRPVARASPTVAISCEAFSAFSLINARA	157
Dib	652	GGAGCATGGGTGGACGTCGGCGGCGAGCAGCTGTGGATCGACGCTCTCCACGCTACGCTG	593
QY	140	GluLysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThr	159

Db
592 GAGCAGCCTCGCGCCCCGGTCTGGACAGACTACCTCCACATCACCGTCGGCGCAG 533

Qy	160	LeuSerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnVal	179
Db	532	CTCTCCAAATGGCGGCATCGGCGGCCAGSCGTTCGGCACGGCGCCAGATCTCCAACGTG	473
Qy	180	LeuGlulLeuAspValIleThrGlyLys-----	188
Db	472	CACGAGCTTGACGTGGTAACAGGTAC-GCCGCGCTCTTGTCTCTGGGCATCGTTTCATGTATA	414
Qy	188	-----	188

Db	413	CATATAATCTGAGAGCTAGCTGTCAATCAACACACCAGTCACAAATGTGTGTCATCGAGCT	354
Qy	189	-----GlyGluMetLeuThrCysSerArgGlnLeuAsn	199
Db	353	GTGTTTGTGTTTTTGGTTGCAGGCACGGGTGAATGGTCAGCTGTTCTCCGGGCAAGAAC	294
Qy	200	ProGluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAla	219
Db	293	TCGGACCTGTTCTACGCAGCATTTGGGTGGGCTGGGTGCAGTTTGGGGTCATAACCCGGGCT	234
Qy	220	ArgIleValLeuSerHisLeuAlaProIleuArgAlaIleValThrPheArgMetLeuTyrSerAsn	239

library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DH10B host cells. Plants were inoculated by Shuxian Li (Glen Hartman lab, University of Illinois). Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois)."

ORIGIN

Alignment Scores: 8.98e-57 Length: 582
Pred. No.: 560.00 Matches: 107
Score: 72.68% Conservative: 34
Percent Similarity: 55.15% Mismatches: 47
Best Local Similarity: 21.57% Indels: 6
Query Match: 12 Gaps: 2
DB:

US-10-014-101-4 (1-501) x BM143498 (1-582)

QY 187 GlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyVal 206
Db 1 GGAAGAGGAGGTTTCGTAACATGCTCTTCACAGAGAACTTGGAGTTATTCACGCGGTT 60
QY 207 LeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAla 225
Db 61 CTTGGAGGCTTGGACAAATTGGAGTTATAGCAAGGCGAGAAATTGCTCTTGAGCCAGCA 120
QY 227 ProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAsp 246
Db 121 CCAAAAGGGTTAAGTGGGTGAGACTACTTTATAGTGACTTTTCTGCTTTTACCAAGAC 180
QY 247 GlnGluArgLeuIleSerMet-----AlaAsnAspIleGlyValAspTyrLeuGlu 263
Db 181 CAGAACGATTATCTCAATCAATGGAAGGAAACAAAGAACGCATTGGATTCTTGGA 240
QY 264 GlyGlnIlePheLeuSerAsnGlyValValAsp-----ThrSerPhePheProPro 280
Db 241 GGGATGCTGTAATGACCAAGGCCCATTAATAATTGGAGATCCTCTTCTCCCTCTA 300
QY 281 SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu 300
Db 301 TCTGACCATCCAGATAGCTTTTAATAACTGAACATAGCATCCTCTACTGCTTGAA 360
QY 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320
Db 361 GTGGCTAAATATTATGACGAACAAACCGAGTTAAATGTGCAAGGAAATTGAAGTTTG 420
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340
Db 421 CTCCAGGACTAGCCTATATCCCTGGATTAAATTATGAGAAAAATGTCGTACGTTGAG 480
QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeu 360
Db 481 TTCTTGAATAGGTCGGAAGTGGAGAGTTGAAACTTCAGTCACAAGGACTGTGGGAAGTT 540
QY 361 ProHisProTrpLeuAsnLeuTyrValProLysSerArgIle 374
Db 541 CCTCACCCGTGGCTTAATTTGTTTATACCAAAATCTCAATC 582

RESULT 14

BE330968

LOCUS

DEFINITION

so91g01.y1 Gm-cl041 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl041-745 5' similar to TR:Q9ZUP1 Q9ZUP1 PUTATIVE CYTOKININ
OXIDASE. ; mRNA sequence.

ACCESSION

BE330968

BE330968 635 bp mRNA linear EST 04-DEC-2001

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source

ORIGIN

Alignment Scores: 2.42e-56 Length: 635
Pred. No.: 557.00 Matches: 110
Score: 69.19% Conservative: 36
Percent Similarity: 52.13% Mismatches: 59
Best Local Similarity: 21.46% Indels: 6
Query Match: 10 Gaps: 2
DB:

US-10-014-101-4 (1-501) x BE330968 (1-635)

QY 171 ArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGlyGlu 190
Db 3 CGTTATGGACCTCAAATCAGCAACGTTCAATGGAATGGATGTCATCATCTGGAAAGGAGAG 62
QY 191 MetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGlyLeu 210
Db 63 TTCGTAACCTTGCTCTTCACAGAAGAACTTGGAGTTATTCACGCGGTTCTTGGAGGCTTA 122
QY 211 GlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLysArgAla 230
Db 123 GGGCAATTTGGAGTTATAGCAAGGCGAGAAATAGCACTTGAGCCAGCCCCCAAGGGTT 182

BE330968.1 GI:9204744
EST.
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 635)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 423.
Location/Qualifiers
1..635
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl041-745"
/tissue_type="Senescing leaves, mature plant, greenhouse
grown"
/lab_host="DH10B"
/clone_lib="Gm-cl041"
/note="Vector: pT7T3Pac (Pharmacia); Site_1: EcoRI;
Site_2: HindIII; This library was constructed from mRNA
isolated from senescing leaf tissue of mature greenhouse
grown plants of the cultivar Williams. Complementary DNA
was synthesized from mRNA using a 3' anchored poly(dT)
primer. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by digestion with EcoRI and
HindIII. The cDNA fragments were directionally cloned
into the EcoRI-HindIII restriction site of the pT7T3-Pac
vector. The ligated cDNA fragments were transformed into
DH10B host cells. This library was constructed by Dr.
Randy Shoemaker."


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Qy 231 LysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArgLeu 250
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183 AAGTGGTCAAGTACTATTATAGTGACTTTTTCGCTTTTACCAAGATCAGGAACGATTA 242
Qy 251 IleSerMet-----AlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePhe 267
|||||
|||:::
243 ATCTCAATCAATGGAAGGAACAAAGAACGCATTGGATTTCTCGAAGGATGCTGCTA 302
Qy 268 LeuSerAsnGlyValValAsp-----ThrSerPhePheProProSerAspGlnSer 284
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303 ATGAACCAAGGCCCCATAAATAATGGAGATCCTCTTCTCCCTCTATCTGACCATCCC 362
Qy 285 LysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyr 304
:::
363 AGAATATCTTCTTTAATAACTGAACATAGCATCCTCTACTGTCTTGAAGTGGCTAAATAT 422
Qy 305 TyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeu 324
|||
423 TATGACGAACAAACCCAGATAAATATGGACAATGAATCAAGTTTGTCTACAGGACTA 482
Qy 325 SerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArg 344
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483 GCCTATATCCCTGTGTTATATTATGAGAAAAACGTGTCACTACGTTGAGTTCTTGAATAGG 542
Qy 345 ValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrp 364
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543 GTCCAAAGAGGACAGGTGGAGCTTCACTCACAAGGACTGTGGATGTTACTCACTCATGG 602
Qy 365 LeuAsnLeuTyrValProLysSerArgIleLeu 375
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603 CTTAATAATGATATATACCAAAAGTCTCGAATCTTG 635
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RESULT 15
BU084470
LOCUS
DEFINITION
sar19h02.y1 Gm-c1049 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1049-7252 5' similar to TR:Q9SU77 Q9SU77 CYTOKININ OXIDASE-LIKE
PROTEIN. ;, mRNA sequence.
ACCESSION
BU084470
VERSION
BU084470.1 GI:22525659
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 566)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
1..566
/organism="Glycine max"
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FEATURES
source

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/db_xref="taxon:3847"
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/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/clone_lib="Gm-c1049"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."
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ORIGIN

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Alignment Scores:
Pred. No.: 3e-56 Length: 566
Score: 555.50 Matches: 109
Percent Similarity: 72.73% Conservative: 27
Best Local Similarity: 58.29% Mismatches: 42
Query Match: 21.40% Indels: 9
DB: 13 Gaps: 3

US-10-014-101-4 (1-501) x BU084470 (1-566)

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Qy 133 AspValLeuLysLysThrAlaGluLysGlyValSerProValSerTrpThrAspTyrLeu 152
|||
64 GATGTGCTACATACCACACTTAAACATGGACTTGCACCAGTTCTTGGACTGATTATTG 123
Qy 153 HisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGlyGlnValPheArgAsn 172
:::
124 TACTTGACCGTGGAGGGACACTTCCCAATGCTGGAATCAGTGGCCAGAGCTTCCGTTAT 183
Qy 173 GlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGlyGluMetLeu 192
|||
184 GGACCTCAATCAGCAACGTTTCATGAAATGGATGTCATCATCGAANAAGGAGATTCGTA 243
Qy 193 ThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGln 212
|||
244 ACTTGCTCTTCACAGAAGAACTTGGAGTTATTTCCACGCGGTTCTTGGAGGCTTAGGGCAA 303
Qy 213 PheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLysArgAlaLysTrp 232
|||
304 TTTGGAGTTATAGCAAGGGCGAGATAGCACTTGAGCCAGCCCCCAAGGGTTAAGTGG 363
Qy 233 PheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArgLeuIleSer 252
|||
364 GTCAGACTACTTTATAGTGACTTTTTTTCGCTTTTACCAAAAGATCAGGAACGATTAATCTCA 423
Qy 253 Met-----AlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePheLeuSer 269
:::
424 ATCAATGGAAGGAAACAAAAGAACGCATTTGGATTTTCTGGAAGGGATGCTGCTAATGAAC 483
Qy 270 AsnGlyValValAsp-----ThrSerPhePheProProSerAspGlnSerLysVal 286
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484 CAAGGCCCCATAAATAATTTGGAGATCCTCTTCTTCCCTCTATCTGACCATCCAGATA 543
Qy 287 AlaAspLeuValLysGlnHis 293
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544 TCTTCTTTAATACTGAACAT 564
Db
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Search completed: April 7, 2004, 10:37:47
Job time : 3800 secs

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6	1822	70.2	1575	9	US-09-938-842A-2089
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22	1060	40.8	1857	14	US-10-326-184-22
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27	993	38.3	1515	14	US-10-014-101-30
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45	745	28.7	1142	12	US-10-424-599-1725

ALIGNMENTS

RESULT 1
US-10-311-453-26
; Sequence 26, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 09:35:37 ; Search time 1742 Seconds
(without alignments)
1077.855 Million cell updates/sec

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Perfect score: 2596
Sequence: 1 MANLRMLITLITVMTKSS.....SKRKDLDPKLLSPGQDIF 501

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delext 7.0

Searched: 2470632 seqs, 1873875610 residues

Total number of hits satisfying chosen parameters: 4941264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description

US-10-311-453-26

Alignment Scores:

Pred. No.: 2.97e-308 Length: 1506
Score: 2596.00 Matches: 501
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-014-101-4 (1-501) x US-10-311-453-26 (1-1506)

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QY	21	AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer	40
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QY	41	IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal	60
Db	121	ATCATCTCGCAGCCTCTCATGACTTCGGAACATAACCCACCGTGACCCCGCGCGGTA	180
QY	61	IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys	80
Db	181	ATCTGCCCTCTCCACCGCTGATATCTCTGCTCTCTCCATAACGCCGCAACGGAAAA	240
QY	81	SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal	100
Db	241	AGTACATTCGAAGTAGCGGCTCGTGGCAAGGCCACTCCTTTAAACGGCCAAGCCTCGTC	300
QY	101	SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys	120
Db	301	TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAGACAAG	360
QY	121	LysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGlu	140
Db	361	AAGTACGCTGACGTGGCGCGGACGTTATGGTGGATGTGCTTAAGAAGACGGCGGAG	420
QY	141	LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeu	160
Db	421	AAAGGGGTGTCGCCGGTTTCTTGGACCGAATATTGTCATATAACCGTCGGAGGAACGTG	480
QY	161	SerAsnGlyGlyIleGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu	180
Db	481	TCGAATGGTGGAAATGGTGGTCAAGTGTTTCGAAACGGTCTCTTGTAGTAACGTCTT	540
QY	181	GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro	200
Db	541	GAATTGGACGTTATTAATCTGGGAAAGGTGAATGTTGACATGCTCGCACAGCTAAACCCA	600
QY	201	GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg	220
Db	601	GAATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGA	660
QY	221	IleValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPhe	240
Db	661	ATTGTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTC	720
QY	241	ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp	260
Db	721	ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGAC	780
QY	261	TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPheProPro	280
Db	781	TATTTAGAAGGTCAAAATATTCTATCAACCGGTGCTGTGACACCTCTTTTCCACCT	840
QY	281	SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu	300
Db	841	TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA	900
QY	301	ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu	320

Db	901	GTAGCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGTTATTGACACATTA	960
QY	321	ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp	340
Db	961	ACGAAAACATTAAGTTACTTTGCCCGGTTTCATATCAATGACAGACGTGGCTACTTCGAT	1020
QY	341	PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu	360
Db	1021	TTCTTGAACCGTGTACATGTCGAAGAAAAATAAACTCAGATCTTTGGGATTATGGGAAC	1080
QY	361	ProHisProTrpLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly	380
Db	1081	CCTCATCCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTCGATTTTCATAACGGT	1140
QY	381	ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro	400
Db	1141	GTTGTCAAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCA	1200
QY	401	ThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp	420
Db	1201	ACAAACCGGAATAATGGGACAATCGTATGTGCGCGATGATACAGAGATCGATGAAGAT	1260
QY	421	ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu	440
Db	1261	GTTATATATATATTCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAG	1320
QY	441	SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr	460
Db	1321	AGCGTTAACGAGAAGATAATTAGGTTTTCGAAGGATTCAGGTATTAAAGATTAAGCAATAT	1380
QY	461	LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp	480
Db	1381	CTAATGCATTATACTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT	1440
QY	481	PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle	500
Db	1441	TTTTCGAAGAGGAAAGATCTATTTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATC	1500
QY	501	Phe 501	
Db	1501	TTT 1503	

RESULT 2

US-10-014-101-26
; Sequence 26, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-26

Alignment Scores: 2.97e-308 Length: 1506
Pred. No.:

Score: 2596.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-014-101-4 (1-501) x US-10-014-101-26 (1-1506)

QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20
Db 1 ATGGCTAATCTTCGTTAATGATCACTTTAATCAAGGTTTAAATGATCAACCAATCATCA 60
QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLysSerThrAspProSer 40
Db 61 AACGGTATTAAATTTGATTACCTAAATCCCTTAACCTCACCCCTCTCTACCGATCCTTCC 120
QY 41 IleIleSerAlaIleAspHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
Db 121 ATCATCTCGCAGCCCTCTCATGACTTCGGAACATAAACCCCGTGACCCCGCGGCGGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80
Db 181 ATCTGCCCTCCTCCCGCTGATATCTCTCGTCTCTCCAATACGCCGCAACGGAAA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
Db 241 AGTACATTCCAAGTAGCGCTCGTGCCCAAGGCCACTCCTTAAACGGCCCAAGCCTCGGTC 300
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys 120
Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGTTCAAAAGACAAG 360
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGlu 140
Db 361 AAGTACGCTGACGTGGCGCGGGACGTTATGGGTGGATGTCTTAAGAAGACGGCGGAG 420
QY 141 LysGlyValSerProValSerThrThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160
Db 421 AAAGGGGTGTCGCCGGTTCTTGGACGGATTATTTGGATATAACCGTCGGAGGAACGTTG 480
QY 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180
Db 481 TCGAATGGTGGAAATTGGTGGTCAAGTGTTTCGAAACCGTCTCTTGTAGTAACGTCCTT 540
QY 181 GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200
Db 541 GAATTGGACGTTATTACTGGGAAGAGTGAAATGTTGACATGCTCGGACAGCTAAACCCA 600
QY 201 GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg 220
Db 601 GAATTGTTCTATGGAGTGTAGGAGGTTTGGGTCAATTTTGGAAATTATAACGAGAGCCAGA 660
QY 221 IleValLeuAspHisAlaProLysArgAlaLysTyrPheArgMetLeuTyrSerAspPhe 240
Db 661 ATTGTTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTC 720
QY 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260
Db 721 ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACAGATATTGGAGTCGAC 780
QY 261 TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePhePro 280
Db 781 TATTTAGAAGGTCAAATATTTCTATCAAACGGTGTGCTTGACACCTCTTTTCCACCT 840
QY 281 SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu 300
Db 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA 900
QY 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320
Db 901 GTAGCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTATTGACACATTA 960
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaLysPheAsp 340

Db 961 ACGAAACATTAAAGTTACTTGGCCGGGTTTCATATCAATGCACGACGTGGCCTACTTCGAT 1020
QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeu 360
Db 1021 TTCTTTGAACCGTGTACATGTGGAAGAAATAAACTCAGATCTTTGGGATTATGGGAAC TT 1080
QY 361 ProHisProTyrLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380
Db 1081 CCTCATCTTGGCTTAACCTCTACGTTCCCTAAATCTCGGATTTCTCGATTTTCATAACGGT 1140
QY 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400
Db 1141 GTTGTCAAAAGACATTCTTCTTAAGCAAAAATCAGCTTCGGGACTCGCTCTCTCTATCCA 1200
QY 401 ThrAsnArgAsnLysTyrAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp 420
Db 1201 ACAAAACCGGAATAAATGGGACAATCGTATGTGCGCGATGATACCAGAGATCGATGAAGAT 1260
QY 421 ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu 440
Db 1261 GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAG 1320
QY 441 SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr 460
Db 1321 AGCGTTAACGAGAAGATAAATAGGTTTTCGAAGGATTCAGGTATTAAAGATTAAAGCAATAT 1380
QY 461 LeuMetHisTyrThrSerLysGluAspTyrIleGluHisPheGlySerLysTyrAspAsp 480
Db 1381 CTAATGCATTATACTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT 1440
QY 481 PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle 500
Db 1441 TTTTTCGAAGAGGAAAGATCTATTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATC 1500
QY 501 Phe 501
Db 1501 TTT 1503

RESULT 3

US-10-326-184-8
; Sequence 8, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-8

Alignment Scores:
Pred. No.: 2,86e-307 Length: 1506
Score: 2588.00 Matches: 500
Percent Similarity: 99.80% Conservative: 0
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 99.69% Indels: 0
DB: 14 Gaps: 0

US-10-014-101-4 (1-501) x US-10-326-184-8 (1-1506)

QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20
Db 1 ATGGCTAATCTTCGTTAATGATCACTTTAATCAGGTTTAAATGATCACCACCAATCATCA 60


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QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40
Db 61 AACGGTATTAAATTGATTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC 120
QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
Db 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATACCAACCGTGACCCCGCGCGGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80
Db 181 ATTCGCCCTCCTCCACCGCTGATATCTCTCGTCTCTCCATACGCCGCAACGGAAAA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
Db 241 AGTACATTCCAAGTAGCGGCTCGTGCCCAAGGCCACTCTTAAACGGCCCAAGCCTCGGTC 300
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys 120
Db 301 TCCGCGGAGTAATCGTCAACATGACGTGTATCATCTGACGTGGTGGTTTCAAAAGACAAG 360
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrPValAspValLeuLysLysThrAlaGlu 140
Db 361 AAGTACGCTGACGTGGCGCGGACGTTATGGTGGATGTGCTTAAGAAGACGCGGAG 420
QY 141 LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160
Db 421 AAAGGGGTGTCGCGGTTTCTTGACGGATTATTTGCATATAACCGTCCGAGGAACGTTG 480
QY 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180
Db 481 TCGAATGGTGGAAATTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACGTCCTT 540
QY 181 GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200
Db 541 GAATTGGACGTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCA 600
QY 201 GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg 220
Db 601 GAATTGTTCTATGGAGTGTAGGAGGTTGGGTCAATTTGGAAATTATAACGAGAGCCAGA 660
QY 221 IleValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPhe 240
Db 661 ATTGTTTGGACCATGCACCTAAACGGSCCAAATGGTTTCGGATGCTCTACAGTGAATTC 720
QY 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260
Db 721 ACAACTTTTACAAAGGACCACCAAGACGTTTGATATCAATGGCAACGATATTGGAGTCGAC 780
QY 261 TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAlaSpThrSerPheProPro 280
Db 781 TATTTAGAAGGTCAAATATTCTATCAACGGTGTGCTGTGACACCTCTTTTTCACCACT 840
QY 281 SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu 300
Db 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA 900
QY 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320
Db 901 GTAGCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTATTGACACATTA 960
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340
Db 961 ACGAAAACATTAAAGTTACTTGGCCGGGTTTCATATCAATGCACGACGTGGCCTACTTCGAT 1020
QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrPValLeu 360
Db 1021 TTCTTGAACCGTGTACATGTGCAAGAAAATAAACTCAGATCTTTGGGATTATGGGAACCT 1080
QY 361 ProHisProTrpLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380
Db 1081 CCTCATCCTTGGCTTAACCTCTACGTTTCTTAAATCTCGGATTCTCGATTTCATAACGGT 1140
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QY 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400
Db 1141 GTTGTCAAAGACATTCTTCTTAAGCAAAATCAGCTTCGGGACTCGCTCTTCTATCCA 1200
QY 401 ThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp 420
Db 1201 ACAAACCGGAATAAATGGGACAATCGTATGTCCGCCGATGATACCAGAGATCGATGAAGAT 1260
QY 421 ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu 440
Db 1261 GTTATATATATATTCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAGTGGAG 1320
QY 441 SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr 460
Db 1321 AGCGTTAAACGAGAAGATAATAGGTTTTTTCGAAGGATTCAGGTATTAAGATTAAGCAATAT 1380
QY 461 LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp 480
Db 1381 CTAATGCATTATACTAGTAAAGAAGATTGGATTGAGCAATTTGGATCAAAATGGGATGAT 1440
QY 481 PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle 500
Db 1441 TTTTCGAAGAGAGAAAGATCTATTGTATCCCAAGAACTGTATTATCTCCAGGCAAGACATC 1500
QY 501 Phe 501
Db 1501 TTT 1503

RESULT 4
US-10-311-453-3
; Sequence 3, Application US/103111453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schilling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-3

Alignment Scores:
Pred. No.: 2,5e-262 Length: 2991
Score: 2226.50 Matches: 499
Percent Similarity: 50.00% Conservative: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 85.77% Indels: 499
DB: 12 Gaps: 4

US-10-014-101-4 (1-501) x US-10-311-453-3 (1-2991)
QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20
Db 1 ATGGCTAATCTTCGTTAATGATCATCTTTAATCACGGTTTTTAATGATCACCAATCATCA 60
QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40
Db 61 AACGGTATTAAAAATGATTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC 120
QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
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Db 121 ATCATCTCGCAGCCTCTCATGACTTCGAAACATAACCAACCGTGACCCCGGGCGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80
Db 181 ATCTGCCCTCCTCCACCGCTGATATCTCTGCTCCTCCAATACGCGCAACGGAAAA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
Db 241 AGTACATTCCAAGTAGCGGCTCGTGGCCAAGGCCACTCCTTAAACGGCCAAGCCTCGGTC 300
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValSerLysAspLys 120
Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGTCTTAAACGGCCAAGCAAG 360
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGlu 140
Db 361 ARGTACGCTGACGTGGCGCGCGGACGTTATGGTGGATGTCTTAAAGAACACGGCGGAG 420
QY 141 LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160
Db 421 AAAGGGGTGTCGCCGTTCTTGGACGGATTATTGTCATATAACCGTCGGAGAACGTTG 480
QY 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180
Db 481 TCGAATGGTGAATGGTGGTCAAGTGTTCGAAACGGTCCTCTTGTTAGTAAACGTCCTT 540
QY 181 GluLeuAspValIleThr----- 186
Db 541 GAATGGACGTTATTACTGTGACGTCATCTTCTAAACTTTGATGTACATACAACAACAAA 600
QY 186 ----- 186
Db 601 ACTGTTTTTGTATTATAGTATTTTTCATTTTTTGTACCATAGGTTTTATGTTTATAGTT 660
QY 186 ----- 186
Db 661 GTGCTAAACTTCTTGCCACACACGTAAGTCTTCGAAACACAAAATGCGTAACGCATCTAT 720
QY 186 ----- 186
Db 721 ATGTTTTTTGTACATATTGAATGTTGTTTCATGAGAAATAAAGTAATTACATATACACACA 780
QY 186 ----- 186
Db 781 TTTATTGTCGTACATATATAATAATAATAAAGACAAATTTTCACAATTGGTAGCGTGTAA 840
QY 186 ----- 186
Db 841 TTTGGGATTTTGTAAATGTACATGCATGACGCATGCATATGGAGCTTTTCGGTTTCTTA 900
QY 186 ----- 186
Db 901 GATTTGTGTAGTATTTCAAATATATCATTTATTTTCTTCGAATAAAGAGGTCGTATATT 960
QY 186 ----- 186
Db 961 TTTAAATAGCAACATTTTCAGAAATTTTCTTTGAATTTACACTTTTAAATTTGTTATTGT 1020
QY 187 -----GlyLysGlyGluMetLeuThrCysSerArgG1 197
Db 1021 TAATATGGATTTTGAATAAATAATTTTCAGGGAAGGTGAATGTTTGACATGCTCCGACACA 1080
QY 197 nLeuAsnProGluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleTh 217
Db 1081 GCTAAACCCAGAAATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAAATTTGGAATTATAAC 1140
QY 217 rArgAlaArgIleValLeuAspHisAlaProLys----- 228
Db 1141 GAGAGCCAGAAATGTTTTGGACCATGCACCTTAAACGGGTACGTATCATATATTTTACCA 1200
QY 228 ----- 228

Db 1201 TTTGTTTTTAGTCAGCATTCATTTTTTCATTAGTAAATCCGTTTCAATTTCTAAATTTTTT 1260
QY 228 ----- 228
Db 1261 AGTCAATAGAAAAATGATCTTTATGTCTAGAGCTTGATTATTTAGTGATTTTATTTAGATA 1320
QY 228 ----- 228
Db 1321 AAATAAAATATAACCTAAACGGAATAATTTATTTACTAATCGGATAATGTCTGATTAAAA 1380
QY 228 ----- 228
Db 1381 CATTTTATGATATTACACTAAGAGAGTTAGAGACGTATGGATCACAAAAACATGAAGCTTT 1440
QY 228 ----- 228
Db 1441 CTTAGATGGTATCCTAAAACTAAAGTTAGGTACAAGTTTGGAAATTTAGGTCAAATGCTTA 1500
QY 228 ----- 228
Db 1501 AGTTGCATTAATTTGAAACAAAATCTATGCAATTGAATAAAAAAAGATATGGATTATTTTA 1560
QY 228 ----- 228
Db 1561 TAAAGTATAGTCCTTGTAAATCCTAGGACTTGTGTCTAATCTTGTCTTATGCGTGCAAAAT 1620
QY 228 ----- 228
Db 1621 CTTTTTGATGTCAATATATAATCCTTGTTTATTAGAGTCAAGCTCTTTCATTAGTCAACT 1680
QY 228 ----- 228
Db 1681 ACTCAAAATATACTCCAAAGTTTAGAATATAGTCTTCTGACTAATTAGAATCTTTACAACCG 1740
QY 228 ----- 228
Db 1741 ATAAACGTTACAATTTGGTTATCATTTTAAAAAACACAGATTTGGTCATAATATACGATGAC 1800
QY 228 ----- 228
Db 1801 GTTCTGTTTTAGTTTCACTATTTCACAAATTTTATATAATATTATTTCAAGAAATATTGA 1860
QY 228 ----- 228
Db 1861 AATACTATACTGTAATATGGTTTCTTTATATATGTGTGTATAAATTAATGGGATTGTTT 1920
QY 229 -----ArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrTh 242
Db 1921 TCTCTAAATGAAATTTGTGTAGGCC-AAATGGTTTCGGATGCTCTACAGTGATTTCACAAC 1979
QY 242 rPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrIle 262
Db 1980 TTTTACAAAGGACCAAGAACGTTGATATCAATGGCAACGATATTGGAGTCGACTATTT 2039
QY 262 uGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAs 282
Db 2040 AGAAGGTCAAATATTTCTATCAAACGGTGTCTGTTGACACCTCTTTTTTCCCACTTCAGA 2099
QY 282 pGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAl 302
Db 2100 TCAATCTAAAGTCGCTGATCTAGTCAAGCAACACCGGTATCATCTATGTTCTTTGAAGTAGC 2159
QY 302 aLysTyrTyrAspAspProAsnLeuProIleIleSerLys----- 315
Db 2160 CAAGTATTATGATGATCCCAATCTCCCATCATCATCAGCAAGGTACTACACATTTACATTTT 2219
QY 315 ----- 315
Db 2220 CATCATCGTTTTTATCATACCATAAGATATTTAAATGATTATTCATTCGCCACCATTAAG 2279
QY 315 ----- 315
Db 2280 ATATTTCATCATCATCGTTACATTTTTTTTTTTTGTGATCTTATGCTTCTCATAATCTACTA 2339

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QY 316 -----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerM 333
Db 2340 TTGTGTAGGTTATTGACACATTAAAGAAACATTAAAGTTACTTGGCCGGGTTTCATATCAA 2399
QY 333 etHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuA 353
Db 2400 TGCACGACGTGGCCTACTTCGATTTCTTGAACCGTGTACATGTGGAAGAAAATAAACTCA 2459
QY 353 rgSerLeuGlyLeuTyrGluLeuProHisProTyrLeuAsnLeuTyrValProLysSera 373
Db 2460 GATCTTTGGGATTATGGGAACCTTCCTCATCTTGGCTTAACCTCTACGTTCCCTAAATCTC 2519
QY 373 rgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAlaS 393
Db 2520 GGATTCTCGATTTTTCATAACGGTGTGTGTCAAAGACATTCTTCTTAAAGCAAAAATCAGCTT 2579
QY 393 erGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405
Db 2580 CGGACTCGCTCTTCTCTATCCCAACAAACCGGAATAA-GTACATACTTCTCTTCATTTCAT 2638
QY 405 ----- 405
Db 2639 ATTATCTTCAAGAACCAAGTAATAAATTTCTATGAACCTGATTATGCTGTATTGTTA 2698
QY 406 --TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleI 425
Db 2699 GATGGACAATCGTATGTGCGGATGATACCCAGAGATCGATGAAGATGTTATATATATATA 2758
QY 425 leGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluL 445
Db 2759 TCGGACTACTACAATCCGCTACCCCAAAGGATCTTCCAGAAGTGGAGACGTTAAACGAGA 2818
QY 445 ysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrT 465
Db 2819 AGATAATTAGGTTTTCGAAGGATTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATA 2878
QY 465 hrSerLysGluAspTyrIleGluHisPheGlySerLysTrpAspPheSerLysArgL 485
Db 2879 CTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGA 2938
QY 485 ysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 2939 AAGATCTATTGATCCCAAGAACTGTTATCTCCAGGCGCAAGACATCTTT 2988

RESULT 5
US-10-014-101-3
; Sequence 3, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-3
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Alignment Scores:
Pred. No.: 25e-262 Length: 2991
Score: 2226.50 Matches: 499
Percent Similarity: 50.00% Conservative: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 85.77% Indels: 499
DB: 14 Gaps: 4

US-10-014-101-4 (1-501) x US-10-014-101-3 (1-2991)

QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20
Db 1 ATGGCTAATCTTCGTTTAATGATCACTTTAATCAGGGTTTAAATGATCACCAAAATCATCA 60
QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40
Db 61 AACGGTATTAAAATTGATTTACCTAAATCCCTTAAACCTCACCTCTCTACCGATCCTTCC 120
QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60
Db 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATAAACACCGTGAACCCCGCGGCGGTA 180
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80
Db 181 ATCTGCCCTCTCTCCACCGCTGATATCTCTCGTCTCTCTCAATACGCCGCAAAACGGAAAA 240
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100
Db 241 AGTACATTCCAAGTAGCGGTCGTGGCCAAGGCCACTCTTAAACGGCCAAGCCTCGGTC 300
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys 120
Db 301 TCCGCGGAGTAATCGTCAACATGACGTGTATCATCGACGTGGTGTTCATAAAGACAAG 360
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGlu 140
Db 361 AAGTACGCTGACGTGGCGGCGGACGTTATGGTGGATGTCTTAAAGAAGACGCGGAG 420
QY 141 LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160
Db 421 AAAGGGGTGTCGCCGGTTTCTTGGACGGATTATTTTGCATATAACCGTCGGAGGAACGTTG 480
QY 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180
Db 481 TCGAATGGTGGAAATTGGTGGTCAAGTGTTTCGAAACGGTCTCTTGTAGTAACGTCCTT 540
QY 181 GluLeuAspValIleThr----- 186
Db 541 GAATTGGACGTTATTACTGGTACGCATCTTCTAAACITTTGATGTACATACAACAACAAA 600
QY 186 ----- 186
Db 601 ACTGTTTTTGTATAGTATTTTTCATTTTTTTGTACCATAGGTTTTTATGTTTATAGTT 660
QY 186 ----- 186
Db 661 GTGCTAAACTTCTTGCAACACACGTAAAGTCTTCGAAACACAAAAATGCGTAACGCATCTAT 720
QY 186 ----- 186
Db 721 ATGTTTTTTGTACATATTGAATGTGTCTTCATGAGAAAATAAAGTAATTACATATACACA 780
QY 186 ----- 186
Db 781 TTTATTGTCGTACATATATAATAATAATAAAGACAAAATTTTCACAATTTGGTAGCGTTAA 840
QY 186 ----- 186
Db 841 TTTGGGATTTTGTAAATGTACATGCATGACGCATGCATATGGAGCTTTTTCGGTTTTCTTA 900
QY 186 ----- 186
Db 901 GATTTGTGTAGTATTTCAAATATATCATTTATTTTCTTTTCGAATAAAGAGGTGTATATT 960
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QY 186 ----- 186
Db TTTAAATAGCAACATTTCAGAAATTTTCTTTGAATTTACACTTTTAAATGTTATTGT 1020
QY 187 -----GlyLysGlyGluMetLeuThrCysSerArgG1 197
Db TAATATGGATTTTGAATAAATAATTTTCAGGGRAAGGTGAAATGTTGACATGCTCGCGACA 1080
QY 197 nLeuAsnProGluLeuPheTyrGlyValLeuGlyGlnPheGlyIleIleTh 217
Db GCTAAACCCAGAAATGTTCTATGGAGTGTAGGAGGTTTGGGTCAATTTGGAATTATAAC 1140
QY 217 rArgAlaArgIleValLeuAspHisAlaProLys----- 228
Db GAGAGCCAGAAATGTTTGGACCATGCACCTAAACGGGTACGTATCATCATATTTTACCA 1200
QY 228 ----- 228
Db TTTGTTTTAGTCAGCATTCATTTTTCATTAGTAATCCGTTTCAATTTCTAAAATTTTTT 1260
QY 228 ----- 228
Db AGTCAATAGAAAATGATCTTATGTCTCAGAGCTTGATATTTTAGTGATTTTATTGAGATA 1320
QY 228 ----- 228
Db AAATAAAATATAACCTAACGGAAATAATTAATTTTACTAATCGGATAATGTCGATTAAAA 1380
QY 228 ----- 228
Db CATTTTATGATATTACACTAAGAGAGTTAGAGACGTATGGATCACAAAACATCAAGCTTT 1440
QY 228 ----- 228
Db CTTAGATGGTATCCTAAAACATAAAGTTAGGTACAAAGTTTGAATTTAGGTCAAAATGCTTA 1500
QY 228 ----- 228
Db AGTTGCATTAATTTGAACAAATCTATGCATTAATAAATAAAGATATGGATTAATTTTA 1560
QY 228 ----- 228
Db TAAAGTATAGTCCTTGTAATCCTAGGACTTGTGTCTAATCTTGTCTTATGCGTGCAAAT 1620
QY 228 ----- 228
Db CTTTTTGATGTCAATATATAATCCTTGTATTATAGAGTCAAGCTCTTTTCATTAGTCAACT 1680
QY 228 ----- 228
Db ACTCAATATACTCCAAAGTTTAGAATATAGTCTTCTGACTAATTAGAATCTTTACAACCG 1740
QY 228 ----- 228
Db ATAAACGTTACAATTTGGTTATCATTTTAAACAAACAGATTTGGTCAATAATATACGATGAC 1800
QY 228 ----- 228
Db GTTCTGTTTAGTTTCATCTATTTCACAAATTTTATATAATTAATTTTCAAGAAATATTGA 1860
QY 228 ----- 228
Db AATACTATACTGTAATATGGTTTCTTTATATATATGTGTGTATATAAATAATGGGATGTTT 1920
QY 229 -----ArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrTh 242
Db TCTCTAAATGAAATTTGTGTAGGCC-AAATGGTTTCGGATGCTCTACAGTGATTTTCACAAC 1979
QY 242 rPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLe 262
Db TTTTACAAAGGACCAAGAACGTTTGTATCAATGGCAACCGAATTTGGAGTCGACTATTT 2039

QY 262 uGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAs 282
Db AGAAGGTCAAATATTTCTATCAAACGGTGTGTCGACACCTCTTTTTTCCACCTTCAGA 2099
QY 282 pGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAl 302
Db TCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGCTATCATCTATGTTCTTGAAGTAGC 2159
QY 302 aLysTyrTyrAspAspProAsnLeuProIleIleSerLys----- 315
Db CAGTATATTATGATGATCCCAATCTCCCATCATCAGCAAGGTACTACACATTACATTTT 2219
QY 315 ----- 315
Db CATCATCGTTTTTATCATACCATAAGATATTTTAAATGATTTCATTGCAACCACATTAAAG 2279
QY 315 ----- 315
Db ATATTTCATCATCATCGTTACATTTTTTTTTTGGCATCTTATGCTTCTCATATATCTACTA 2339
QY 316 -----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerM 333
Db TTGTGTAGGTTATTGACACATAACGAAACATTAAAGTTACTTGCCTGGGTTTCATATCAA 2399
QY 333 etHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuA 353
Db TGCACGACGTGGCCTACTTCGATTTCTTTGAACCGGTGTACATGTGGAAGAAATAAACTCA 2459
QY 353 rgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSerA 373
Db GATCTTTGGGATTATGGGAATCTTCTCATCTTGGCTTAACCTCTACGTTCCATAATCTC 2519
QY 373 rgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAlaS 393
Db GGATTTCTCGATTTTTCATAACGGTGTGTCAAAGACATTTCTTTAAAGCAAAATCAGCTT 2579
QY 393 erGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405
Db CGGGACTCGCTCTTCTCTATCCAAACAAACCGGAATAA-GTACATACTTCTCTTCATTCA 2638
QY 405 ----- 405
Db ATTTATCTTCAAGAACCAAGTAAATAAATTTTCTATGAAGTATGTTATGTTATTGTTA 2698
QY 406 --TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleI 425
Db GATGGGACAATCGTATGTGCGCGATGATACCAGAGATCGATGAAGATGTTATATATATA 2758
QY 425 leGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluL 445
Db TCGGACTACTACAATCCGCTACCCAAAGGATCTTCCAGAGTGGAGAGCGTTAACGAGA 2818
QY 445 ysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrT 465
Db AGATAATTAGGTTTTCGAAGGATTCAGGTATTAAGATTAAGCAATATCTAATGCATTATA 2878
QY 465 hrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArgL 485
Db CTAGTAAAGAAGATTGGATTGGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGA 2938
QY 485 ysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db AAGATCTATTGATCCCAAGAACTGTTATCTCCAGGGCAACACATCTTT 2988

RESULT 6

US-09-938-842A-2089
; Sequence 2089, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2089
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2089

Alignment Scores:
Pred. No.: 4.47e-213 Length: 1575
Score: 1822.00 Matches: 345
Percent Similarity: 80.08% Conservative: 69
Best local Similarity: 66.73% Mismatches: 79
Query Match: 70.18% Indels: 24
DB: 9 Gaps: 5

US-10-014-101-4 (1-501) x US-09-938-842A-2089 (1-1575)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
Db 25 CTCATCACCTTAATAACGCTTTTATAGTTTAAACCCCAACCTTAATCAAATCAGATGAG 84
QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
Db 85 GGCATTGATGTTTCTTACCCCATATCACTCAACCTTACGGTCCTAACCGATCCCTTCTCC 144
QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61
Db 145 ATCTCTGCCGCTTCTCACGACTTCGTTAAACATAACCGACGAAATCCCGGCCGCTCTC 204
QY 62 CysProSerThrAlaAspIleSerArgLeuLeuGlnThrAlaAlaAsnGly----- 79
Db 205 TGCCCTTCTCCACCACGAGGTGGTGGTCTCTCCTCCGTTTCGCTAACCGAGGATCTCT 264
QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db 265 TACAATAAAGGCTCAACAGCCCGCTACTTTCAAAGTGGTGTCTCGAGGCCAAGGC 324
QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
Db 325 CACTCCCTCCGTGCCAAGCCTCTGCACCGGAGGTGTCGTCTGTAACATGACGTGTCTC 384
QY 112 -----ThrAspValValSerLysAspLysLysThrAlaAspVal 125
Db 385 GCCATGGCGGCTAAACAGCGGCTGTATCTCGGCAGACGGGACTTACGCTGACGTG 444
QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145
Db 445 GCTGCCGGACGATGTGGTGGATGTTCTGAAGCGCGGTGGATAGAGCGGTCTCTCGCCG 504
QY 146 ValSerTrpThrAspThrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
Db 505 GTTACATGGACGGATTATTGTATCTCAGCGTCGGCGGACGTTGTGGAACGCTTGAATC 564
QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185
Db 565 GGTGGTCAGACGTTTAGACACAGCCCTCAGATTAGTAACGTTTCATGACGTTGACGTTAT 624
QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGlnLeuPheThrGly 205
Db 625 ACCGAAAGGTGAATGATGACTTGCTCTCCAAAGTTAAACCTGATTTCTTATATGGA 684
QY 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaAlaArgIleValLeuAspHis 225

Db 685 GTTTAGGAGGTTTGGGTCAATTCCGTTATTATACGAGGGCCAGGATTGCGTTGGATCAT 744
QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTrpSerAspPheThrThrPheThrLys 245
Db 745 GCACCCACAAGGTTGAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA 804
QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspThrLeuGluGlyGln 265
Db 805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTGGAGGTCAA 864
QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285
Db 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTTTCTCCACTCTCCGATCAACAAGA 924
QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleThrValLeuGluValAlaLysThrTyr 305
Db 925 GTCCGATCTCTTGTGAATGACCAACCGGATCATCTATGTTCTCGAAGTAGCCAACTATTAT 984
QY 306 AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer 325
Db 985 GACAGAACCAACCTTCCCATTTATGACCAGGTGATGACACGTTAAGTAGAACTTAGGT 1044
QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaLysPheAspPheLeuAsnArgVal 345
Db 1045 TTCGCTCCAGGGTTTATGTTTCGTACAAGATGTTCCGTTATTCGATTCTTGAACCGTGT 1104
QY 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365
Db 1105 CGAAACGAAGAAGATAAATCAGATCTTTAGGACTATGGGAAGTTCTCTCATCCATGCTT 1164
QY 366 AsnLeuTrpValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385
Db 1165 AACATCTTGTCCCGGGTCTCGAATCCAAGATTTTTCATGATGGTGTATTATAATGGCCTT 1224
QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTrpProThrAsnArgAsnLys 405
Db 1225 CTTCTAAACCAAAACCTCAACTTCTGCTGTTACTCTCTTCTATCCCAACCGAAACAAA 1284
QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleThrIleIle 425
Db 1285 TGGAAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTATGTGATC 1338
QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAATCTCAACGAC 1398
QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnThrLeuMetHisThr 464
Db 1399 AAGGTTATTGAGTTTGTGAAAACTCGGGAATTAAGATTAAAGGAATATTGATGCACTAT 1458
QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484
Db 1459 ACAAGAAAGAGATTTGGTTAAACATTTTGGACCAAAATGGGATGATTTTTTAAGAAAG 1518
QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1519 AAAATTATGTTTATCCCAAAAGACTATTGTCTCCAGGACAAGACATATTT 1569

RESULT 7

US-09-938-842A-2089
; Sequence 2089, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24

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; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2089
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2089

Alignment Scores:
Pred. No.:      4,47e-213      Length:      1575
Score:          1822.00      Matches:      345
Percent Similarity: 80.08%      Conservative: 69
Best Local Similarity: 66.73%      Mismatches: 79
Query Match:      70.18%      Indels:      24
DB:              11          Gaps:         5

US-10-014-101-4 (1-501) x US-09-938-842A-2089 (1-1575)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 CTCATCACCCCTAATAACGCTTTTATAAGTTTAAACCCCAACCTTAATCAAAATCAGATGAG 84

QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 GGCATTGATGTTTTCTTACCCATATCACTCAACCTTACGGTCCTAAACCGATCCCTTCTCC 144

QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 145 ATCTGCGGCTTCTCACGACTTCGGTAACATAACCGACGAAATCCCGGCCCGCTCTCTC 204

QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 205 TGCCCTTCTCCACCCACGAGGTGGCTCGTCTCTCCGTTTCGCTAACGGAGGATTTCTCT 264

QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 265 TACAATAAAGGCTCAACCGCCGCTCTACTTTCAAAGTGGCTGCTCGAGGCCAAGGC 324

QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 325 CACTCCCTCCGTGGCCCAAGCCTCTGCACCCGGAGGTGTCGTCGTGAACATGACGTGCTC 384

QY 112 -----ThrAspValValSerLysAspLysLysTyrAlaAspVal 125
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 385 GCCATGCGGCTAAACCGCGGCTGTTATCTCGGCACACGGGACTTACGCTGACGTG 444

QY 126 AlaAlaGlyThrLeuTrpValaspValLeuLysLysThrAlaGluLysGlyValSerPro 145
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 445 GCTGCCGGGACGATGTGGTGGATGTTCTGAAGCGCGCGGTGGATAGAGCGGCTCTCGCCG 504

QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 505 GTTACATGACGGATTATTTGTATCTCAGCGTCGGCGGGACGTTGTTCGAACGCTGGAATC 564

QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 565 GGTGGTCAGACGTTTAGACACCGGCCCTCAGATTAGTAACGTTTCATGACGTTATT 624

QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 625 ACCGAAAAGGTGAAATGATGACTTGGCTCTCCAAAGTTAAACCCCTGAATTGTTCTATGGA 684

QY 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 685 GTTTTAGGAGGTTTGGGTCAATTCCGTTATTATAACGAGGCCAGGATTGCGTTGGATCAT 744

QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Db 745 GCACCCACAAGGGTGAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA 804

QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGln 265
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 805 GACCAAGAGCGTTTAATATCAATGACCAATGATCTCGGAGTTGACTTTTGAAGGTCAA 864

QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTCTCCCACTCTCCGATCAACAAGA 924

QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyr 305
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 925 GTCGCATCTCTTGTGAATGACCACCGGATCATCTATGTTCTCGAAGTAGCAAGTATTAT 984

QY 306 AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer 325
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 985 GACAGAACCCCTTCCCATTTATTGACCAGGTGATTGACACGTTAAGTAGAACTCTAGGT 1044

QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1045 TTCGCTCCAGGGTTTATGTTCTGTAAGATGTTCCGATTTTCGATTTCTTGAAACCGTGT 1104

QY 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1105 CGAAACGAAGAGATAAACTCAGATCTTTTAGGACTATGGGAAGTTCTCTCATCCATGGCTT 1164

QY 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1165 AACATCTTTGTCCCGGGTCTCGAATCCAAGATTTTCATGATGGTGTATTATTAATGGCCTT 1224

QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1225 CTTCTAAACCAACCAACCTCACTTCTGGTGTACTCTCTTATCCCAACCCGAAACAAA 1284

QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1285 TGGAAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTATGTGATC 1338

QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAACTTGAAATCTCAACGAC 1398

QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1399 AAGTTATTGAGTTTGTGAAAACCTCGGGAATTAAAGATTAAAGGAATATTTGATGCACTAT 1458

QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg 484
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1459 ACAAGAAAAGAGATTGGGTTAAACATTTTGGACCAAAATGGGATGATTTTTTAAAGAAAG 1518

QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1519 AAAATTATGTTTGTATCCCAAAAGACTATTGTCTCCAGGACACACATATTT 1569

RESULT 8
US-10-311-453-28
; Sequence 28, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-28

Alignment Scores:
Pred. No.:      4,47e-213      Length:      1575
Score:          1822.00      Matches:      345
Percent Similarity: 80.08%      Conservative: 69
Best Local Similarity: 66.73%      Mismatches: 79
Query Match:      70.18%      Indels:      24
DB:              12          Gaps:          5

US-10-014-101-4 (1-501) x US-10-311-453-28 (1-1575)

QY      7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
Db      25 CTCATCACCTTAATAACGCTTTTATAAGTTTAAACCCCAACCTTAATCAAATCAGATGAG 84

QY      22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLysSerThrAspProSerIle 41
Db      85 GGCATTGATGTTTCTTACCCATATCACTCAACCTTACGGTCTAAACCGATCCCTTCTCC 144

QY      42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61
Db      145 ATCTCTGCCGTTCTCACGACTTCGGTTAACATAACCGACGAAATCCCGCGCCGTCCTC 204

QY      62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
Db      205 TGCCCTTCTCCACACGAGGTGGCTGCTCTCCTCCGTTTCGCTAACGGAGGATTCTCT 264

QY      80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db      265 TACAATAAAGGCTCAACACGAGCCCGGCTGCTACTTTCAAAGTGGTGCTCGAGGCCAAGGC 324

QY      92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
Db      325 CACTCCCTCCGTGGCCAAAGCCTCTGCACCGGAGGTGTCGTCGTGAACATGACGTGTC 384

QY      112 -----ThrAspValValSerLysAspLysLysTyrAlaAspVal 125
Db      385 GCCATGGCGGCTAAACACGAGCGGCTGTTGTTATCTCGGACAGCGGACTTACGCTGACGTG 444

QY      126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145
Db      445 GCTGCCGGACGATGGTGGTGATGTTCTGAAGCGCGGCTGGTGGATAGAGCGCTCTCGCCG 504

QY      146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
Db      505 GTTACATGACGCGATTATTGTATCTCAGCGTCGGCGGACGTTGTCGAACGCTGGAATC 564

QY      166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185
Db      565 GGTGGTCAGACGTTTAGACACGCGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTTATT 624

QY      186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205
Db      625 ACCGAAAGGTGAATGATGACTTGCTCTCCAAAGTTAAACCCCTGATTTGTTCTATGGA 684

QY      206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaAlaArgIleValLeuAspHis 225
Db      685 GTTTTAGGAGGTTTGGGTCAATTCCGGTATTATACGAGGGCCAGGATTGCGTTGGATCAT 744

QY      226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrLys 245
Db      745 GCACCCACAAGGGTGAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA 804

QY      246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGlyGln 265
Db      805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTTCGAAGGTCAA 864
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QY      266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285
Db      865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTTTCTCCACTCTCCGATCAAACAAGA 924

QY      286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305
Db      925 GTCGCATCTCTTGTGAATGACACCGGATCATCTATGTTCTCGAAGTAGCCAAGTATTAT 984

QY      306 AspAspProAsnLeuProIleLeuSerLysValIleAspThrLeuThrLysThrLeuSer 325
Db      985 GACAGAACCCACCTTCCCATTTATGACCAGGTGATTGACAGCTTAAGTAGAACTCTAGGT 1044

QY      326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345
Db      1045 TTCGCTCCAGGGTTTATGTTTCGTACAAAGATGTTCCGTATTTCGATTTCTTGAACCCGTGC 1104

QY      346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365
Db      1105 CGAAACGAAAGAGATAAACTCAGATCTTTAGGACTATGGGAAGTTCTCTCATCCATGGCTT 1164

QY      366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385
Db      1165 AACATCTTTGTCCTCCGGGTCTCGAATCCAAGATTTTTCATGATGGTGTATTATTAATGGCCTT 1224

QY      386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405
Db      1225 CTTCTAAACCAAACTCAACTTCTGGTGTACTCTCTTCTATCCCAAAACCGAAACAA 1284

QY      406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425
Db      1285 TGGAAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTTATGTGATC 1338

QY      426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db      1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAATCTCAACGAC 1398

QY      445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHistyr 464
Db      1399 AAGGTTATTCACTTTGTGAAACTCGGAATTAAGATTAAAGGAATATTGTGACACTAT 1458

QY      465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg 484
Db      1459 ACAAGAAAGAGATGGGTAAACATTTGGACCAAAATGGGATGATTTTAAAGAAAG 1518

QY      485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db      1519 AAATTATGTTTGAATCCCAAGACTATTGTCTCCAGGACAAGACATATTT 1569

RESULT 9
US-10-014-101-28
; Sequence 28, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1575
; TYPE: DNA
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ORGANISM: Arabidopsis thaliana
US-10-014-101-28
Alignment Scores:
Pred. No.: 4.47e-213 Length: 1575
Score: 1822.00 Matches: 345
Percent Similarity: 80.08% Conservatives: 69
Best Local Similarity: 66.73% Mismatches: 79
Query Match: 70.18% Indels: 24
DB: 14 Gaps: 5
US-10-014-101-4 (1-501) x US-10-014-101-28 (1-1575)
QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
Db 25 CTCATCACCCCTAATAACGCTTTTATAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84
QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
Db 85 GGCATTGATGTTTCTTACCCATATCACTCAACCTTACGGTCCCTAACCGATCCCTTCTCC 144
QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61
Db 145 ATCTCTGCCGCTTCTCAGACTTCGGTAAACATAACCGACGAAATAATCCCGCGCTCTCTC 204
QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
Db 205 TGCCCTTCTCCACCACCGAGGTGGCTCTCTCCTCGTTTCGTTAACGGAGGATTCTCT 264
QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db 265 TACAATAAGGCTCAACACGCCCCGGCTGTACTTTCAAAGTGGTGTCTCGAGGCCAAGGC 324
QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
Db 325 CACTCCCTCCGTGGCCAAAGCCTCTGCACCGGAGGTGTCTCGTAAACATGACGTGTCTC 384
QY 112 -----ThrAspValValSerLysAspLysLysTyrAlaAspVal 125
Db 385 GCCATGGCGGCTAAACACGCGGGTGTGTATCTCGGACAGCGGACTTACGTCGACGTG 444
QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145
Db 445 GCTGCCGGGACGATGGTGGTGGATGTTCTGAAGCGCGGCGGTGGATAGAGCGCTCTCGCCG 504
QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
Db 505 GTTACATGGACGATATTATTTGTATCTCAGCGTCGGCGGACGTTGTCTGAACGCTGGAATC 564
QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185
Db 565 GGTGGTCAAGCGTTAGACACGCGCCCTCAGATTAGTAACTTCACTGAGCTTGACGTTATT 624
QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205
Db 625 ACCGAAAAGGTGAATATGATGACTTGCTCTCCAAAGTTAAACCCCTGAATTGTTCTATGGA 684
QY 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225
Db 685 GTTTTAGGAGGTTGGGTCAATTCCGGTATTATAACGAGGCCAGGATTGCGTTGGATCAT 744
QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245
Db 745 GCACCCACAAGGGTGAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA 804
QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGln 265
Db 805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTGAAGGTCAA 864
QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285
Db 865 CTTATGATGTCAATGGCTTCGTAGACACCTCTTCTTCTCCCACTCTCCGATCAACAAGA 924

QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305
Db 925 GTCGCATCTCTTGTGAATGACCACCGGATCATCTATGTTCTCGAAGTAGCCAAATATTAT 984
QY 306 AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer 325
Db 985 GACAGAACCACCCCTTCCCATTTATTGACCAGGTGATTGACACGTTAAGTAGAACTTAGGT 1044
QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345
Db 1045 TTCGTCACAGGTTTATGTTCTCGTACAGATGTTCCGTATTTCCGATTCTTGAACCGTGT 1104
QY 346 HisValGluGlnAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365
Db 1105 CGAAACGAAGAGATAAACTCAGATCTTTAGGACTATGGGAAGTTCTCATCCATGGCTT 1164
QY 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385
Db 1165 AACATCTTTGTCGGGGTCTCGAATCCAGATTTTCATGATGGTGTATTATTAATGGCCTT 1224
QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405
Db 1225 CTTCTAAACCAACCTCAACTTCTGGTGTACTCTCTTCTATCCACAAACCGAAACAAA 1284
QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425
Db 1285 TGGAAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTATGTGATC 1338
QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAATCTCAACGAC 1398
QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHistyr 464
Db 1399 AAGTTATTTCAGTTTGTGAAAACTCGGGAATTAAGATTAAAGGAATATTGATGCACAT 1458
QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg 484
Db 1459 ACAAGAAAAGAGATTGGTTAAACATTTTGACCAAAATGGGATGATTTTTTAAGAAAG 1518
QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1519 AAAATTATGTTTGATCCCAAAAGACTATTGTCTCCAGGACAAGACATATTT 1569

RESULT 10

US-10-326-184-20
; Sequence 20, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C)
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-20

Alignment Scores:
Pred. No.: 4.86e-213 Length: 1655
Score: 1822.00 Matches: 345
Percent Similarity: 80.08% Conservatives: 69
Best Local Similarity: 66.73% Mismatches: 79
Query Match: 70.18% Indels: 24
DB: 14 Gaps: 5

US-10-014-101-4 (1-501) x US-10-326-184-20 (1-1655)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
Db 25 CTCATCACCCCTAATAACGCTTTTATAAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84
QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
Db 85 GGCATTGATGTTTCTTACCCCATATCACTCAACCTTACGGTCTCTAACCGATCCCTTCTCC 144
QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61
Db 145 ATCTCTGCCGTTCTCAGGACTTCGGTAACATAACCGACGAAATCCCGCGCGCTCCTC 204
QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
Db 205 TGCCCTTCTCCACCGAGGTGGCTCGTCTCTCCGTTTCGCTAACGGAGGATTCTCT 264
QY 80 -----LysSerThrPheGlnValAlaAlaAlaArgGlyGlnGly 91
Db 265 TACAATAAAGGCTCAACGAGCCCCGCGTCTACTTTCAAAGTGGCTGCTCGAGGCCAAGGC 324
QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
Db 325 CACTCCCTCCGTGGCCAGCCTCTGCACCCGGAGGTGTCGCTGTAACATGACGTGTCTC 384
QY 112 -----ThrAspValvalSerLysAspLysLysTyrAlaAspVal 125
Db 385 GCCATGGCGGCTAAACGAGCGGCGTGTGTTATCTCGGCAGACGGGACTTACGCTGACGTG 444
QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145
Db 445 GCTGCCGGGACGATGTGGTGATGTTCTGAAGCGCGCGTGGATAGAGCGGTCTCGCCG 504
QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
Db 505 GTTACATGGACGGATTATTGTATCTCAGCGTCGGCGGACGTTGTTCGAACGGCTGGAATC 564
QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185
Db 565 GGTGGTCAGACGTTTAGACACAGGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTTATT 624
QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205
Db 625 ACCGAAAAGGTGAATGATGACTTGCTCTCCAAAGTTAAACCCCTGAATTGTTCTATGGA 684
QY 206 ValLeuGlyGlyLeuGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225
Db 685 GTTTTAGAGGTTTGGGTCAATTCCGTATTATAACGAGGGCCAGGATTGCGTTGGATCAT 744
QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245
Db 745 GCACCCACAAGGGTGAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA 804
QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGln 265
Db 805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTGAAGGTCAA 864
QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285
Db 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTTCTCCCACTCTCCGATCAACAAGA 924
QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305
Db 925 GTCGCATCTCTTGTGAATGACCACCGGATCATCTATGTTCTCGAAGTAGCCAAGTATTAT 984
QY 306 AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer 325
Db 985 GACAGAACCACCCCTTCCATTATTGACCAGGTGATTGACACGTTTAAGTAGAACTCTAGGT 1044
QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345
Db 1045 TTGCTCCAGGGTTTATGTTTCGTACAAGATGTTCCGTATTTCGATTTCCTTGAACCGTGT 1104

QY 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365
Db 1105 CGAAACGAAGAAGATAAACTCAGATCTTTAGGACTATGGGAAGTTCTCTCATCCATGGCTT 1164
QY 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValVallyAspIle 385
Db 1165 AACATCTTGTCCCGGCTCTCGAATCCAAGATTTTCATGATGGTGTATTATAATGGCCTT 1224
QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405
Db 1225 CTTCTAAACCAACCTCAACTTCTGGTGTACTCTCTTATCCCAACACCGAAACAAA 1284
QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425
Db 1285 TGAACAACACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTATGTGATC 1338
QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAATCTCAACGAC 1398
QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db 1399 AAGGTTATTAGTTTTGTGAAAACTCGGGAATTAAGATTAAAGGAATATTGATGCACATAT 1458
QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484
Db 1459 ACAAGAAAAGAGATTGGTTAAACATTTTGGACCAAAATGGGATGATTTTAAAGAAAG 1518
QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1519 AAAATTATGTTTGATCCCAAAAGACTATTGTCTCCAGGACAAAGACATATTT 1569

RESULT 11

US-10-326-184-10
; Sequence 10, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-10

Alignment Scores:
Pred. No.: 7.88e-213 Length: 1575
Score: 1820.00 Matches: 345
Percent Similarity: 79.88% Conservative: 68
Best Local Similarity: 66.73% Mismatches: 80
Query Match: 70.11% Indels: 24
DB: 14 Gaps: 5

US-10-014-101-4 (1-501) x US-10-326-184-10 (1-1575)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
Db 25 CTCATCACCCCTAATAACGTTTTTTTATAAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84
QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
Db 85 GGCATTGATGTTTCTTACCCCATATCACTCAACCTTACGGTCTCTACCGATCCCTTCTCC 144
QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61

Db 145 ATCTCTGCGCTTCTCAGACTTCGGTAACATAACCGACGAAATCCCGCGCGTCTCTC 204
Qy 62 CysProSerSerThralaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
Db 205 TGCCCTTCTCCACCGAGGTGGCTCGTCTCTCTCGTTTCGTTAACGGAGATTCTCT 264
Qy 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db 265 TACAATAAAGGCTCAACCGAGCCCGCGTCTACTTTCAAAGTGGCTGCTCGAGGCCAAGC 324
Qy 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyValIleValAlaAsnMetThrCysIle 111
Db 325 CACTCCCTCCGTGGCCAAAGCTCTGCACCGGAGGTGTCGTGTAACATGACGTGTCTC 384
Qy 112 -----ThrAspValValValSerLysAspLysLysTyrAlaAspVal 125
Db 385 GCCATGGCGGCTAAACCGCGCGGTGTTATCTCGGCAGACGGGACTTACGCTGACGTG 444
Qy 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145
Db 445 GCTGCCGGGACGATGTGGGTGGATGTTCTGAAGCGCGGTGGATAGAGGCGTCTCGCCG 504
Qy 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
Db 505 GTTACATGGACGGATTATTGTATCTCAGCGTCGGCGGACGTTGTTCGAACGCTGAATC 564
Qy 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185
Db 565 GGTGGTCAGACGTTTAGACACGGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTTAT 624
Qy 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205
Db 625 ACCGAAAAGGTGAATGATGACTTGTCTCCAAAGTTAAACCCCTGAATTGTCTATGA 684
Qy 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225
Db 685 GTTTAGGAGGTTTGGGTCAATCGGTATTATAACGAGGCCAGGATTGCGTTGGATCAT 744
Qy 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245
Db 745 GCACCCACAAGGGTGAAATGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTAAAGA 804
Qy 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGlyGln 265
Db 805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTGGAGGTCAA 864
Qy 266 IlePheLeuSerAsnGlyValValAspThrSerPheProProSerAspGlnSerLys 285
Db 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTTCTCCACTCTCCGATCAACAAGA 924
Qy 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305
Db 925 GTCGCATCTCTTGTGAATGACACCGCGGATCATCTATGTTCTCGAAGTAGCCAAAGTATTAT 984
Qy 306 AspAspProAsnLeuProIleLeSerLysValIleAspThrLeuThrLysThrLeuSer 325
Db 985 GACAGAACCAACCTTCCCATTTATGACAGGTGATTGACAGGTTAAGTAGAACTCTAGGT 1044
Qy 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345
Db 1045 TTCGCTCCAGGGTTTATGTTTCGTACAAGATGTTCCGTATTTCGATTCTTGAACCGTGC 1104
Qy 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365
Db 1105 CGAAACGAAGAAGATAAACTCAGATCTTTAGGACTATGGGAAGTTCCTCATCCATGGCTT 1164
Qy 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385
Db 1165 AACATCTTTGTCGGGGTCTCGAATCCAAGATTTTCATGATGGTGTATTATATGGGCTT 1224
Qy 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405

Db 1225 CTTCTAAACCAACCTCAACTTCTGGTGTACTCTCTTATCCCAACCGAAACAAA 1284
Qy 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425
Db 1285 TGAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTATGTGATC 1338
Qy 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTGGCAAGAACTTGAAATCTCAACGAC 1398
Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db 1399 AAGTTATTTCAGTTTTTGAAAACTCGGGAATTAAAGATAATTATGATGCACTAT 1458
Qy 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484
Db 1459 ACAAGAAAAGAGATTGGGTTAAACATTTTGGACCAAAATGGGATGATTTTTTAAGAAAG 1518
Qy 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1519 AAAATTATGTTTGATCCCAAAAGACTATTGTCTCCAGGACAAGACATATTT 1569

RESULT 12
US-10-311-453-7
; Sequence 7, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-7

Alignment Scores:
Pred. No.: 6.25e-178 Length: 2782
Score: 1539.50 Matches: 344
Percent Similarity: 44.89% Conservative: 69
Best Local Similarity: 37.39% Mismatches: 80
Query Match: 59.30% Indels: 429
DB: 12 Gaps: 9

US-10-014-101-4 (1-501) x US-10-311-453-7 (1-2782)

Qy 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21
Db 25 CTCATCACCTAATAACGCTTTTATAGTTTAAACCCCAACCTTAATCAAATCAGATGAG 84
Qy 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41
Db 85 GGCATTGATGTTTTCTTACCCATATCACTCAACCTTACGCTCTTAACCGATCCCTTCTCC 144
Qy 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61
Db 145 ATCTCTGCGCTTCTCACGACITTCGGTAACATAACCGACGAAAATCCCGCGCGTCTC 204
Qy 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
Db 205 TGCCCTTCTCTCCACCGAGGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 264

QY	80	-----LysSerThrPheGlnValAlaAlaArgGlyGlnGly	91
Db	265	TACAATAAAGGCTCAACCGCCCGCGTCTACTTTCAAAGTGGCTGCTCGAGGCCAAGGC	324
QY	92	HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle	111
Db	325	CACTCCCTCCGTGGCCCAAGCCTCTGCACCGGAGGTGTCGTGAACATGACGTGTCTC	384
QY	112	-----ThrAspValValSerIysAspLysLysTyrAlaAspVal	125
Db	385	GCCATGGCGGCTAAACCGCGCGGTGTTATCTCGGCAGACGGGACTTACGCTGACGTG	444
QY	126	AlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGluLysGlyValSerPro	145
Db	445	GCTGCGGACGATGTGGTGGATGTTCTGAAGCGCGCGGTGGATAGAGCGGTCTCGCCG	504
QY	146	ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle	165
Db	505	GTTACATGGACGGATTATTGTATCTCAGCGTCGCGCGGACGTTGTGGAACGCTGGAATC	564
QY	166	GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle	185
Db	565	GGTGGTCAGACGTTTAGACACGCGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTATT	624
QY	186	Thr-----	186
Db	625	AC-CGGTACGTAAATACCAAACTTCACTAATCTCGTTACAATTTTAAATTTTGGTA	683
QY	186	-----	186
Db	684	ATATAAATTTGTACGGCTCAACTCTTAATTAAGAATGAACAGTATCTATGATCTCTA	743
QY	186	-----	186
Db	744	GATGCTCTTTTGTCTGCAAGCTTTAATTGTAGTAACATCAGCGATATATATATACACA	803
QY	186	-----	186
Db	804	TGCATGTGTATTATTGATGATAATATATAATGTTTGTAGTTACAAATTTGATTCTCAAGT	863
QY	186	-----	186
Db	864	AAACTCACACGCCATAACCAAGTATAAACTCCAAAATCACGTTTGGTCAGAAATACA	923
QY	186	-----	186
Db	924	TATCCTTCAATTAACAGTAGTTATGCTATAAATTGTGATTATAAATAACTCCGGAGTTGT	983
QY	187	-----GlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro	200
Db	984	TCACAATACTAAATTCAGGAAAAGGTGAATGATGACTTGCTCTCCAAAAGTTAAACCCCT	1043
QY	201	GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg	220
Db	1044	GAATGTCTCTATGGAGTTTGTAGGAGTTTGGGTCAATTTCGGTATTATAACGAGGGCCAGG	1103
QY	221	IleValLeuAspHisAlaProLys-----	228
Db	1104	ATTGCGTTGGATCATGCACCCACAAAGGTATGTATCATCATCTATAGTGTAAATCAATTT	1163
QY	228	-----	228
Db	1164	ATAATTTTAATGTAGTGTCTCTAAATCCAAAATTTGATTGATTGTTGGTGAACGTACGT	1223
QY	228	-----	228
Db	1224	ATATATAATAAGTCAAAAGGCTGATTTTGAAGACGAATTTATATACCTTTTGTGAATTA	1283
QY	228	-----	228
Db	1284	ATCTGATTTTGTCTTACGTTTATTAGATTCTGCGTAATAAAATCCTAGGACTTGCTCGAGT	1343

QY	228	-----	228
Db	1344	GTAATCTTGTCTTATGCTTGCAAAATCTTGTGATGTCAAATATCTAATCTTTTATTATA	1403
QY	228	-----	228
Db	1404	TTTCCCTACGTAAGTTTTAGATATAGTTATTTTAAACTGCTATAAAATTTGTGTACGTATAG	1463
QY	228	-----	228
Db	1464	ACTTTAGATAAAAAAGTTGTGTCGCTTGCACTATTGTTTATCGCTATAGTATGATTCAAA	1523
QY	228	-----	228
Db	1524	GGTCTATATATGATTCTTGTGTTTTCTTTTGAATAAATAAGACCATACAATCCAAAGAA	1583
QY	229	-----ArgAlaLys	231
Db	1584	GATGATCTTAAATGGACTAATTTATGGATATAAAATGATATACAAATCTGCAGGTG-AAA	1642
QY	232	TrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArgLeuIle	251
Db	1643	TGGTCTCGCATACTCTACAGTACTTCTCGGCTTTTAAAGAGACCAAGAGCGTTTAATA	1702
QY	252	SerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePheLeuSerAsnGly	271
Db	1703	TCAATGACCAATGATCTCGGAGTTGACTTTTGGAAAGGTCAACTTATGATGTCAAATGGC	1762
QY	272	ValValAspThrSerPhePheProSerAspGlnSerLysValAlaAspLeuValLys	291
Db	1763	TTCGTAGACACCTCTTCTTCCCACTCTCCGATCAACAAGAGTGCATCTCTTGTGAAT	1822
QY	292	GlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsnLeuPro	311
Db	1823	GACCACCGGATCATCTATGTTCTCGAAGTAGCCAAAGTATTATGACAGAACCCCTTCCC	1882
QY	312	IleIleSerLys-----	315
Db	1883	ATTATTGACCCAGGTACTAAATCCATTATTTCATGATGATTATCTTCACACAATCAGTATC	1942
QY	315	-----	315
Db	1943	ATCACCAAATTACCATCATCACTTGTCTATATATGATCCAAAGTAAATATATCACATGATAT	2002
QY	315	-----	315
Db	2003	AAATAAATCGTTCAAATCTTTT-----TAAAGAATAAAGAATCATTTTCAAGCATTACTC	2062
QY	315	-----	315
Db	2063	ATACACATCTACGAATCACCGTGACCATATATAACCATACGCTTATTAAATAATCATTTT	2122
QY	316	-----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSer	332
Db	2123	TGTTTGTAGGTGATTGACACGTTAAGTAGAATCTAGGTTTCGCTCCAGGGTTTATGTTT	2182
QY	333	MetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeu	352
Db	2183	GTACAAGATGTTCCGTTATTTTCGATTCTTGAACCGTGTCCGAAACGAAGAAGATAAACTC	2242
QY	353	ArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSer	372
Db	2243	AGATCTTTTAGGACTATGGGAAGTTCTCTCATCCATCGGCTTAAACATCTTTTCCCGGGTCT	2302
QY	373	ArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAla	392
Db	2303	CGAATCCAAGATTTTCATGATGATGTTTATTATAAGCCCTTCTTCTAAACCAACCTCAACT	2362
QY	393	SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys-----	405
Db	2363	TCTGTGTACTCTCTTCTATCCCAACCGAACAAGTAATAATTTACTTTTGTGATTT	2422
QY	405	-----	405

Db 2423 TGTTTTATTGAAAGTATATCCCAATATATGTATGTTAAATGTTAAACAAGAAATTTATTTT 2482

QY 406 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValile 422

Db 2483 ATTAATAGATGGAAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTT 2536

QY 423 TyrIleIleGlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSer 441

Db 2537 TATGTGATCGGAATTAATGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAAGAACTTGAAAT 2596

QY 442 ValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeu 461

Db 2597 CTCAACGACAAGGTATTTCAGTTTGTGAAAACCTCGGGAATTAAGATTAAAGGAATATTG 2656

QY 462 MethIstYrThrSerLysGluAspTyrIleGluHisPheGlySerLysTrpAspAspPhe 481

Db 2657 ATGCACATATACAGAAAAGAAGATTGGGTTAAACATTTTGGACCAAAATGGGATGATTTT 2716

QY 482 SerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501

Db 2717 TTAAGAAAAGAAATATGTTTGTATCCCAAAAGACTATTGTCTCCAGGACAAGACATATTT 2776

RESULT 13

US-10-014-101-7

; Sequence 7, Application US/10014101

; Publication No. US20030074698A1

; GENERAL INFORMATION:

; APPLICANT: Schmulling, Thomas

; APPLICANT: Werner, Tom s

; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and

; TITLE OF INVENTION: physiology

; FILE REFERENCE: 1195-2

; CURRENT APPLICATION NUMBER: US/10/014,101

; CURRENT FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: PCT/EP01/06833

; PRIOR FILING DATE: 2001-06-16

; PRIOR APPLICATION NUMBER: EP 00870132.8

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: US 60/258,415

; PRIOR FILING DATE: 2000-12-27

; PRIOR APPLICATION NUMBER: EP 01870053.4

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 2782

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-10-014-101-7

Alignment Scores:

Pred. No.:	6.25e-178	Length:	2782
Score:	1539.50	Matches:	344
Percent Similarity:	44.89%	Conservative:	69
Best Local Similarity:	37.39%	Mismatches:	80
Query Match:	59.30%	Indels:	429
DB:	14	Gaps:	9

US-10-014-101-4 (1-501) x US-10-014-101-7 (1-2782)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21

Db 25 CTCATCACCCCTAATAACGCTTTTATAAGTTTAAACCCCAACCTTAATCAAAATCAGATGAG 84

QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41

Db 85 GGCATTGATGTTTTCTTACCATATCACTCAACCTTACGGTCCTAAACCGATCCCTTCTCC 144

QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValile 61

Db 145 ATCTGCGCGTCTCTCAGCACTTCGGTTAACAATAACCGACGAAATCCCGGCGCGTCTCTC 204

QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79

Db 205 TGCCCTTCCTCCACACGAGGTGGCTCGTCTCCTCGTTTCGCTAACGGAGGATTCTCT 264

QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91

Db 265 TACAATAAAGGCTCAACACGCCCCGCTCTACTTTCAAAGTGGCTGCTCGAGGCCAAGGC 324

QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111

Db 325 CACTCCCTCCGTGGCCAAGCCTCTGCACCCGAGGTGTCTGCTGTAACATGACGTGTCTC 384

QY 112 -----ThrAspValValSerLysAspLysLysValSerLysValAlaAspVal 125

Db 385 GCCATGGCGGCTAAACACGCGGCTTGTATCTCGGCAGACGGGACTTACGTCACGTG 444

QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145

Db 445 CCTGCCGGGACGATGGGTGGATGTTCTGAAGCGCGGTGGATAGAGCGGTCTCGCCG 504

QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165

Db 505 GTTACATGGACGGATTATTGTATCTCAGCGTCGGCGGACGTTGTTCGACCGCTGGAATC 564

QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValile 185

Db 565 GGTGGTCAGACGTTTAGACACGGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTTATT 624

QY 186 Thr----- 186

Db 625 AC-CGGTACGTAAATACCAAAACTTCACTAAATCTCGTTACAAATTTTAAATTTTGGTA 683

QY 186 ----- 186

Db 684 ATATAAAATTTGTACGGCTCAACTCTTAATTAAAGAAATGAACAGTATCTATGATCTTCTA 743

QY 186 ----- 186

Db 744 GATGCTCTTTTGTCTGCAAGCTTTTAATTGTAGTAACATCAGCGATATATATATACACA 803

QY 186 ----- 186

Db 804 TGCATGTGATTATTATGATGATAATAATAATAGTTTGTAGTTACAAATTTGATTCTCAAGGT 863

QY 186 ----- 186

Db 864 AAAACTCACACGCCCATACACAGTATAAAAACCTCCAAAAATCACGTTTGGTCAGAAATACA 923

QY 186 ----- 186

Db 924 TATCCTTCATTAAACAGTAGTATGCTATAATTTGTGATTATAAATAAATCCTCCGAGTTTGT 983

QY 187 -----GlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200

Db 984 TCACAATACTAAATTTTCAGGAAAAAGGTGAATGATGACTTGCTCTCCAAAGTTAAACCCCT 1043

QY 201 GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg 220

Db 1044 GAATTGTTCTATGGAGTTTAGGAGGTTTGGGTCAATTTCGGTATTATAACGAGGSCCAGG 1103

QY 221 IleValLeuAspHisAlaProLys----- 228

Db 1104 ATTGCGTTGGATCATGCAACCCCAAGGATGATGATCATGTCATCTATAGTGTATCAATTT 1163

QY 228 ----- 228

Db 1164 ATAATTTTAATGTAGTGGTCTCTAAATCCAAATTTGATTGATTGTTGGTGAACGTACGT 1223

QY 228 ----- 228

Db 1224 ATATATAAAGTCAAAAGGCTGATTTTGAAGACGAATTTATATACTTTTGTGTAATTA 1283

QY 228 ----- 228

Db 1284 ATCTGATTTTGCTTACGTTTATTAGATTCTGCGTAATAAATCCTAGGACTTGCTCGAGT 1343
QY 228 ----- 228
Db 1344 GTAATCTTGCTTATGCTTGCAAAATCTTGTTGATGTCAAATATCTAATCTTTTATTATA 1403
QY 228 ----- 228
Db 1404 TTTCCCTACGTAAGTTTATAGATATAGTTATTTTAAACTGCTATAAAATTGTTGACGTATAG 1463
QY 228 ----- 228
Db 1464 ACTTTAGATAAAAAAGTTTGTCGCTTGACCTATTGTTTATCGCTATAGTATCAAA 1523
QY 228 ----- 228
Db 1524 GGTCTATATATGATCTCTGAGTCTCTCGGCTTTTAAAGAGACCAAGCGTTTAATA 1702
QY 252 SerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePheLeuSerAsnGly 271
Db 1703 TCAATGACCAATGATCTCGGAGTTGACTTTTGGAGGTCAACTTATGATGTCAAATGGC 1762
QY 272 ValValAspThrSerPheProProSerAspGlnSerLysValAlaAspLeuValLys 291
Db 1763 TTCGTAGACACCTCTTTCTCCCACTCTCCGATCAACAAGAGTCGCATCTCTTGTAAT 1822
QY 292 GlnHisGlyIleIleTyrValIleuGluValAlaLysTyrTyrAspAspProAsnLeuPro 311
Db 1823 GACCACCGGATCATCTATGTTCTCGAAGTAGCCAAAGTATTATGACAGAACCACCCCTTCCC 1882
QY 312 IleIleSerLys----- 315
Db 1883 ATTATTGACCAGGTACTAAATCCATTATTTCATGATGATTATCTTCACACATCAGTATC 1942
QY 315 ----- 315
Db 1943 ATCACCAAATTACCATCATCTGTCATATATGATCCAAAGTAAATATATCATGATAT 2002
QY 315 ----- 315
Db 2003 AAATAAATCGTTCAAATCTTTTAAAGAAATAAAGAATCATTTTCAAGCATTACTC 2062
QY 315 ----- 315
Db 2063 ATACACATCTACGAATCACCGTGACCATATATAACCATACGCTTATTAATAATCATTTT 2122
QY 316 -----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSer 332
Db 2123 TGTTGTAGGTGATTGACACGTTAAGTAGAACTCTAGGTTTCGCTCCAGGGTTTATGTTT 2182
QY 333 MetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeu 352
Db 2183 GTACAAGATGTTCCGTATTTCGATTCTTGAACCGTGTCCGAAACGAAGAAGATAAACTC 2242
QY 353 ArgSerLeuGlyLeuTyrPheGluLeuProHisProTrpLeuAsnLeuTyrValProLysSer 372
Db 2243 AGATCTTTAGGACTATGGGAAGTTCCTCATCCATGGCTTAACATCTTTGTCCCGGGTCT 2302
QY 373 ArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAla 392
Db 2303 CGAATCCAAGATTTTCATGATGGTGTATTAAATGGCCTTCTTCTAAACCAAACTCAACT 2362
QY 393 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405

Db 2363 TCTGGTGTACTCTCTTCTATCCCAAAACCAGAAAGTAAATATTTACTTTTGTATT 2422
QY 405 ----- 405
Db 2423 TGTTTTATTGAAAGTATATCCCAATAATGTATGTATAAATTTGTTAAACAAGATTTATTT 2482
QY 406 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIle 422
Db 2483 ATTAATAGATGGAACAACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTT 2536
QY 423 TyrIleIleGlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSer 441
Db 2537 TATGTGATCGGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAAT 2596
QY 442 ValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeu 461
Db 2597 CTCAACGACAAGGTTATTTCAGTTTGTGAAAACCTCGGAATTAGATTAAAGGAATATTG 2656
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QY 482 SerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 2717 TTAAGAAAGAAATTTATGTTGATCCCAAAAGACTATTGTCTCCAGGACACACATATT 2776
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US-10-311-453-27
; Sequence 27, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-27
Alignment Scores:
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Score: 1292.00 Matches: 251
Percent Similarity: 69.05% Conservative: 106
Best Local Similarity: 48.55% Mismatches: 138
Query Match: 49.77% Indels: 22
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Db 373 GTAAACCGGGATCGAGGTATCAAGGTGTCTAGGACCTGTTTATATATGTGACGTGGACGCT 432
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Db 433 GCGTGGCTATGGATTGAGGTGTTGAATAAACTTTGGAGTTAGGTTAAGCGTAAACGGGTTTCT 492
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QY 168 GlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly 187
Db 553 CAAACGTTTCGGTACGTCACAGATCACTAATGTTCTAGAGATGGATGTTATTACTGA 612
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QY 228 LysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGln 247
Db 733 AAAAGGGCCAAAGTGGTTAAGGTTTCTATACATAGATTTCTCCGAATTCACAAGAGATCAA 792
QY 248 GluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePhe 267
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QY 268 LeuSerAsnGlyValValAsp-----ThrSerPhePheProProSerAspGlnSer 284
Db 847 GTGGACCATGGCCACCAGGATAAAGTGGAGATCCAGGTATTATCCACCGTCCGATCACTTG 906
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Db 907 AGGATCGCCTCAATGGTCAAAACGACATCGTGTCACTACTGCCTTGAAGTCGTCAAGTAT 966
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QY 345 ValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeuProHisProTyr 364
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QY 365 LeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAsp 384
Db 1147 CTTAATCTCTTCGTACCAAAACTCAAATCTCCAAATTTGATGATGGTGTGTTTAAGGGT 1206
QY 385 IleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsn 404
Db 1207 ATTATCTAAGAAATAACATCACTAGCGGTCCTGTTCTTGTGTTTATCCTATGAATCGCAAC 1266

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Db 1267 AAGTGAATGATCGGATGTCTGCCGTATATACCCGAG-----GAAGATGATTTTATGCG 1320
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Db 1321 GTAGGGTTTTTAAGATCCGCGGGTTTTGACAAATGGGAGGCTTTTGATCAAGAAACATG 1380
QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
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Db 1501 AAATATAATATGATCCCAAAATGATATATATATATATATATATTT 1551

RESULT 15

US-10-014-101-27
; Sequence 27, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-27

Alignment Scores:

Pred. No.: 6.31e-148 Length: 1572
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Percent Similarity: 69.05% Conservative: 106
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Query Match: 49.77% Indels: 22
DB: 14 Gaps: 6

US-10-014-101-4 (1-501) x US-10-014-101-27 (1-1572)

QY 3 AsnLeuArgLeuMetIleThrIleIleThr-----ValLeuMetIleThrLysSer 19
Db 13 AATCTCGTTCACAAGTTCGTCTTATAGCAATAACAATAGTAAATCATCATTAATCTCTCA 72
QY 20 SerAsnGlyIleLysIleAspLeuProLysSerLeuAsnLeu----- 33
Db 73 ACTCCGATCACAAACCAACACATCACCAACCATGGATATCTTTTCACACAACGAATTC 132
QY 34 -----ThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsn 51
Db 133 GCCGGAAAACTCACCTCCTCCTCCTCCTCGTCCGATCAGCCGCCACAGATTTCCGCCAC 192
QY 52 IleThrThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSerArg 71
Db 193 GTCACCAAAATCTTCCCTTCCGCGGTCTTAATCCCTTCTCCGTTGAAGACATCACAGAT 252

Qy 425 IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1321 GTAGGGTTTTTAAGATCCGCGGGTTTTTGACAATTGGGAGGCTTTTGTATCAAGAAAACATG 1380
Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
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Qy 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484
Db 1441 TCATCACAGAAGGATGGGTTAGACATTTTGTCCGAGGTGGAATATTTTCGTAGAGAGA 1500
Qy 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
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Search completed: April 7, 2004, 12:30:47
Job time : 1781 secs

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Db 373 GTAAACCGGGATCGAGGTATCAAGGTGTCTAGGACCTGTTTATATGTTGACGTGGACGCT 432
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GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1506	100.0	1687	8	BT004107	BT004107 Arabidops
5	1504.4	99.9	1506	8	AF303978	AF303978 Arabidops
6	778.2	51.7	1575	6	AX339731	AX339731 Sequence
7	778.2	51.7	1575	6	AX507394	AX507394 Sequence
8	778.2	51.7	1575	6	AX651615	AX651615 Sequence
9	778.2	51.7	1575	6	AX785079	AX785079 Sequence
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11	778.2	51.7	1655	8	BT000179	BT000179 Arabidops
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21	318.6	21.2	1602	6	AR399216	AR399216 Sequence
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ACCESSION	AX339729					
VERSION	AX339729.1	GI:18135722				
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SOURCE	Arabidopsis thaliana (thale cress)					
ORGANISM	Arabidopsis thaliana					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi					
REFERENCE	1					
AUTHORS	Schmueling, T. and Werner, T.					
TITLE	Method for modifying plant morphology, biochemistry and physiology					

JOURNAL Patent: WO 0196580-A 26 20-DEC-2001;
Schmullling, Thomas (DE) ; Werner, Tomas (DE)
Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 100.0%; Score 1506; DB 6; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGGCTAATCTTCGTTTAATGATCACTTTAATCACGGTTTAAATGATGATCACCAGAAATCATCA 60
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DEFINITION Sequence 26 from Patent WO03050287.
ACCESSION AX785077
VERSION AX785077.1 GI:32952908
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS Schmullling, T. and Werner, T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 03050287-A 26 19-JUN-2003;
Schmullling, Thomas (DE) ; Werner, Tomas (DE)
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RESULT 3
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LOCUS Arabidopsis thaliana clone U20989 mRNA linear PLN 15-MAR-2003
DEFINITION Arabidopsis thaliana clone U20989 putative cytokinin oxidase
(At2g19500) mRNA, complete cds.
ACCESSION BT005653
VERSION BT005653.1 GI:28973496
KEYWORDS FLI CDNA.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1537)

REFERENCE
AUTHORS Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wong,C., Wu,H.C.,
Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M.,
Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,
Ecker,J.R. and Theologis,A.
Arabisopsis Open Reading Frame (ORF) Clones
Unpublished
2 (bases 1 to 1537)

TITLE
JOURNAL
REFERENCE
AUTHORS Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M.,
Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,
Ecker,J.R. and Theologis,A.
Direct Submission

TITLE
JOURNAL
COMMENT Submitted (15-MAR-2003) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and

sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.

FEATURES source

Location/Qualifiers
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3'UTR

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Db 1501 TTTTGA 1506

RESULT 4

BT004107

LOCUS

DEFINITION

Arabidopsis thaliana clone RAFL15-29-H04 (R20989) putative cytochrome oxidase (At2g19500) mRNA, complete cds.

ACCESSION

BT004107

VERSION

BT004107.1

KEYWORDS

FLI CDNA.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1687)

Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Arabidopsis Full Length cDNA Clones

Unpublished

2 (bases 1 to 1687)

Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Direct Submission

Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.

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RESULT 5
 AF303978
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 ACCESSION AF303978
 VERSION AF303978.1 GI:11120507
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 1506)
 AUTHORS Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.

TITLE A family of cytokinin oxidases from Arabidopsis thaliana
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1506)
 AUTHORS Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and Morris, R.O.

TITLE Direct Submission
 JOURNAL Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall, Columbia, MO 65211, USA

FEATURES
 source Location/Qualifiers
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AX339731
LOCUS AX339731 1575 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 28 from Patent WO0196580.
ACCESSION AX339731
VERSION AX339731.1 GI:18135724
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Schmuelling, T. and Werner, T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 0196580-A 28 20-DEC-2001;
Schmuelling, Thomas (DE); Werner, Tomas (DE)
FEATURES
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Best Local Similarity 72.2%; Pred. No. 1.8e-210;
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LOCUS AX507394 1575 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 2089 from Patent WO0216655.
ACCESSION AX507394
VERSION AX507394.1 GI:23388631
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
TITLE Stress-regulated genes of plants, transgenic plants containing same, and methods of use
JOURNAL Patent: WO 0216655-A 2089 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG (CH)
FEATURES
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Best Local Similarity 72.2%; Pred. No. 1.8e-210;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;
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LOCUS			
DEFINITION			
Sequence 428 from Patent WO03000898.			
ACCESSION			
AX651615			
VERSION			
AX651615.1 GI:29154433			
KEYWORDS			
Arabidopsis thaliana (thale cress)			
SOURCE			
ORGANISM			
Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE			
AUTHORS			
Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,			
Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.			
Plant genes involved in defense against pathogens			
Patent: WO 0300898-A 428 03-JAN-2003;			
Syngenta Participations AG (CH)			
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location/Qualifiers			
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ORIGIN			
Query Match			
Best Local Similarity			
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51.7%; Score 778.2; DB 6; Length 1575;			
72.2%; Pred.No. 1.8e-210;			
0; Mismatches 363; Indels 57; Gaps 4;			
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RESULT 9
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LOCUS AX785079 1575 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 28 from Patent WO03050287.
ACCESSION AX785079
VERSION AX785079.1 GI:32952910
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Schmulling, T. and Werner, T.
TITLE Method for modifying plant morphology, biochemistry and physiology
JOURNAL Patent: WO 03050287-A 28 19-JUN-2003;
Schmulling, Thomas (DE); Werner, Tomas (DE)
FEATURES
source location/Qualifiers
1..1575
/organism="Arabidopsis thaliana"
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ORIGIN
Query Match 51.7%; Score 778.2; DB 6; Length 1575;
Best Local Similarity 72.2%; Pred. No. 1.8e-210;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;
QY 42 AATGATCACCATAATCATCAACGGTATTAATAATGATTTTACCTAAATCCCTTAACCTCAC 101
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Db 1557 ACAAGACATATTT 1569

RESULT 12
AY054460

LOCUS
DEFINITION
Arabidopsis thaliana cytochrome oxidase-like protein (At4g29740;
T16L4.250) mRNA, complete cds.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE
AUTHORS

Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

Direct Submission
Submitted (28-AUG-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

TITLE
JOURNAL

COMMENT

e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

Location/Qualifiers

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ORIGIN

Query Match

51.7%; Score 778.2; DB 8; Length 1863;

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LOCUS

DEFINITION Arabidopsis thaliana chromosome 2 clone F3P11 map C1C06E08, complete sequence.

ACCESSION AC005917

VERSION AC005917.3 GI:20197478

KEYWORDS HTG.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 92822)

AUTHORS Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E., Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.-I., Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D., Nierman,W.C., Fraser,C.M. and Venter,J.C.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 92822)

AUTHORS Lin,X.

TITLE Direct Submission

JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

REFERENCE 3 (bases 1 to 92822)

AUTHORS Town,C.D. and Kaul,S.

TITLE Direct Submission

JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org

COMMENT On Apr 18, 2002 this sequence version replaced gi:6598497.

FEATURES

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repeat_region

repeat_region

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Query Match      38.3%;   Score 577;   DB 8;   Length 92822;
Best Local Similarity 75.9%;   Pred. No. 1.5e-152;
Matches 852;   Conservative 0;   Mismatches 40;   Indels 231;   Gaps 2;

QY 615 AGTGTAGGAGGTTTGGGTCAATTTGGAAATTATAACGAGAGCCAGAAATGTTTTGGACCA 674
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Db 40172 ACTGTAATATGTTCTTATATATGTGTGTAAATTAATGGGATTGTTTCTCTAAA 40113

QY 675 TGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTACAACTTTTACAAA 734
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40112 TGAATTTGTAGGCCAAATGGTTTCGGATGCTCTACAGTGATTTACAACTTTTACAAA 40053

QY 735 GGACCAAGAACGTTTGATATCAATGGCAAACGATATTGGAGTCGACTATTAGAAAGGTCA 794
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Db 40052 GGACCAAGAACGTTTGATATCAATGGCAAACGATATTGGAGTCGACTATTAGAAAGGTCA 39993

QY 795 AATATTTCTATCAAACGGTGTGTTGACACCGTCCTTTTCCCACCTTCAGATCAATCTAA 854
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Db 39992 AATATTTCTATCAAACGGTGTGTTGACACCGTCCTTTTCCCACCTTCAGATCAATCTAA 39933

QY 855 AGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCAAGTATTA 914
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Db 39932 AGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCAAGTATTA 39873

QY 915 TGATGATCCCAATCTCCCATCATCAGCA-----943
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 39872 TGATGATCCCAATCTCCCATCATCAGCAAGGTAACACATTTTACATTTTCATCATCGT 39813

QY 944 -----943
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Db 39752 ATCATCATCGTTACATTTTTTTGATCTTATGCTTCTCATAACTACTATTGTGTAGG 39693

QY 947 TTATGTACACATTAAACGAAAAACATTAAAGTTACTTCCCGGGTTTCATATCAATGCACGACG 1006
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Db 39692 TTATGTACACATTAAACGAAAAACATTAAAGTTACTTCCCGGGTTTCATATCAATGCACGACG 39633

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Db 39632 TGGCCTACTTCGATTTCTTTGAACCGGTGATACATGTCGAAGAAAAATAAATCAGATCTTTGG 39573

QY 1067 GATTATGGGAACCTTCTCATCTTTGGCTTAACTCTACGTTCTTAAATCTCGGATCTCTCG 1126
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Db 39572 GATTATGGGAACCTTCTCATCTTTGGCTTAACTCTACGTTCTTAAATCTCGGATCTCTCG 39513

QY 1127 ATTTTCATAACCGGTGTTGTCAAAGACATTTCTTTTAAGCAAAAAATCAGCTTCGGACTCG 1186
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QY 1187 CTCTTCTCTATCCAACAAACCGGAATA-----1214
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QY 1215 -----ATGGGACAA 1223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 39392 AAGAACCAAGTAAATAATTTCTATGAACCTGATATGCTGTGTTATGTTAGATGGGACAA 39333

QY 1224 TCGTATGTCGGCGATGATACAGAGATCGATGAAGATGTTATATATATATATTCGGACTACT 1283
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QY 1284 ACAATCCGCTACCCCAAAGGATCTTCAGAAAGTGGAGAGCGTTAACGAGAAGATAATTAG 1343
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QY 1344 GTTTTGCAAGGATTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATAGTAAAGA 1403
Db |||||
39212 GTTTTGCAAGGATTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATAGTAAAGA 39153
QY 1404 AGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATT 1463
Db |||||
39152 AGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATT 39093
QY 1464 TGATCCCAAGAAACTGTTATCTCCAGGCAAGACATCTTTTGA 1506
Db |||||
39092 TGATCCCAAGAAACTGTTATCTCCAGGCAAGACATCTTTTGA 39050

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Job time : 6061 secs

OM nucleic - nucleic search, using sw model

Run on: April 6, 2004, 20:36:10 ; Search time 691 Seconds
(without alignments)
9258.736 Million cell updates/sec

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Perfect score: 1506
Sequence: 1 atggctaattcttcgtttaat.....cagggaagacatcttttga 1506

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1506	100.0	1506	6	ABK28625	Abk28625 cDNA enco
2	1506	100.0	1506	8	ACC85294	Acc85294 Arabidops
3	1454	96.5	1548	3	AAC43214	Aac43214 Arabidops
4	778.2	51.7	1575	3	AAC42983	Aac42983 Arabidops
5	778.2	51.7	1575	6	ABZ14284	Abz14284 Arabidops
6	778.2	51.7	1575	6	ABK28627	Abk28627 cDNA enco
7	778.2	51.7	1575	7	ADA68648	Ada68648 Arabidops
8	778.2	51.7	1575	8	ACC85296	Acc85296 Arabidops
9	577	38.3	2991	6	ABK28607	Abk28607 DNA encod
10	577	38.3	2991	8	ACC85276	Acc85276 Arabidops
11	470	31.2	1572	6	ABK28626	Abk28626 cDNA enco
12	470	31.2	1572	8	ACC85295	Acc85295 Arabidops
13	461.2	30.6	503	3	AAC36788	Aac36788 Arabidops
14	318.6	21.2	1602	2	AAX02919	Aax02919 Z. mays c
15	306.2	20.3	1611	6	ABK28628	Abk28628 cDNA enco
16	306.2	20.3	1611	8	ACC85297	Acc85297 Arabidops
17	306.2	20.3	1620	6	ABK28632	Abk28632 cDNA enco
18	306.2	20.3	1620	8	ACC85301	Acc85301 Arabidops
19	248.8	16.5	1728	6	ABK28624	Abk28624 cDNA enco
20	248.8	16.5	1728	8	ACC85293	Acc85293 Arabidops
21	238.2	15.8	1566	7	ADA71115	Ada71115 Rice gene
22	232	15.4	1587	7	ADA69574	Ada69574 Rice gene
23	225.8	15.0	2782	6	ABK28609	Abk28609 DNA encod

24	225.8	15.0	2782	8	ACC85278	Acc85278 Arabidops
25	209	13.9	1590	7	ADA69773	Ada69773 Rice gene
26	185.2	12.3	1605	2	AAX02914	Aax02914 Z. mays c
27	183.4	12.2	1593	7	ADA69430	Ada69430 Rice gene
28	181	12.0	1608	3	AAC86501	Aac86501 DNA encod
29	172	11.4	3302	6	ABK28608	Abk28608 DNA encod
30	172	11.4	3302	8	ACC85277	Acc85277 Arabidops
31	171	11.4	1515	6	ABK28629	Abk28629 cDNA enco
32	171	11.4	1515	8	ACC85298	Acc85298 Arabidops
33	144.4	9.6	1677	7	ADA70177	Ada70177 Rice gene
34	123.8	8.2	2805	6	ABK28610	Abk28610 DNA encod
35	123.8	8.2	2805	8	ACC85279	Acc85279 Arabidops
36	123.8	8.2	2814	6	ABK28631	Abk28631 DNA encod
37	123.8	8.2	2814	8	ACC85300	Acc85300 Arabidops
38	108.2	7.2	6733	2	AAX02913	Aax02913 Z. mays c
39	84	5.6	84	6	ABK28630	Abk28630 A. thalia
40	84	5.6	84	8	ACC85299	Acc85299 Arabidops
41	73.8	4.9	1936	6	ABK28611	Abk28611 DNA encod
42	73.8	4.9	1936	8	ACC85280	Acc85280 Arabidops
43	73.2	4.9	2236	6	ABK28606	Abk28606 DNA encod
44	73.2	4.9	2236	8	ACC85275	Acc85275 Arabidops
45	53.6	3.6	1464	7	ABT32136	Abt32136 Benzodiaz

ALIGNMENTS

RESULT 1
ABK28625
ID ABK28625 standard; cDNA; 1506 BP.
XX
AC ABK28625;
XX
XX
DT 09-APR-2002 (first entry)
XX
XX
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX2.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
XX
PA (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX
DR WPI; 2002-130736/17.
XX
XX
PT Polynucleotide encoding novel plant protein having cytokinin oxidase
PT activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
XX
PS Claim 2; Page 146-147; 154pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a novel
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for
CC production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;

enhancing the formation of lateral or adventitious roots; altering root geotropism, leading to an increase in yield; and for screening growth promoting chemical of herbicides. (I) is useful for increasing the size of the root meristem; increasing root size; increasing the size of the shoot meristem; delaying leaf senescence and altering leaf senescence; increasing leaf thickness; reducing or increasing the vessel size; inducing parthenocarp; improving standability of the seedlings; increasing branching and for improving lodging resistance. Antibody (III) to (II) is useful for identifying and obtaining proteins interacting with (II) comprising a screening assay, preferably a two-hybrid screening assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase coding sequences and PCR primers of the invention

Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;
Query Match 100.0%; Score 1506; DB 6; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	AACGGTATTAAATGATTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC	120
Db	61	AACGGTATTAAATGATTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC	120
QY	121	ATCATCTCCGAGCCTCTCATGACTTCGGAACATAACCAACCGTGACCCCGCGGCGTA	180
Db	121	ATCATCTCCGAGCCTCTCATGACTTCGGAACATAACCAACCGTGACCCCGCGGCGTA	180
QY	181	ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCTCTCCCAATACGCCGCAACGGAAA	240
Db	181	ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCTCTCCCAATACGCCGCAACGGAAA	240
QY	241	AGTACATCCCAAGTAGCGGTCGTGGCCAAAGGCCACTCTTAAACGGCCAAAGCGTTC	300
Db	241	AGTACATCCCAAGTAGCGGTCGTGGCCAAAGGCCACTCTTAAACGGCCAAAGCGTTC	300
QY	301	TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGTGTTTCAAAAGACA	360
Db	301	TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGTGTTTCAAAAGACA	360
QY	361	AAGTACGTGACGTGGCGGCGGACGTTATGGGTGGATGCTTAAAGAGACGGCGGAG	420
Db	361	AAGTACGTGACGTGGCGGCGGACGTTATGGGTGGATGCTTAAAGAGACGGCGGAG	420
QY	421	AAAGGGGTCTCGCGGTTTCTTGACGGATTATTTGCAATATAACCGTCGGAGGACGTTG	480
Db	421	AAAGGGGTCTCGCGGTTTCTTGACGGATTATTTGCAATATAACCGTCGGAGGAACGTTG	480
QY	481	TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCCTCTTGTAGTAACGTCCTT	540
Db	481	TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCCTCTTGTAGTAACGTCCTT	540
QY	541	GAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGCGACAGCTAAACCCA	600
Db	541	GAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGCGACAGCTAAACCCA	600
QY	601	GAATTGTTCTATGAGTGTAGGAGGTTTGGGTCAATTTGGAAATATAACGAGAGCCAGA	660
Db	601	GAATTGTTCTATGAGTGTAGGAGGTTTGGGTCAATTTGGAAATATAACGAGAGCCAGA	660
QY	661	ATTGTTTGGACCATGCACCTAAACGGGCGCAAAATGGTTTCGGATGCTCTACAGTGATTC	720
Db	661	ATTGTTTGGACCATGCACCTAAACGGGCGCAAAATGGTTTCGGATGCTCTACAGTGATTC	720
QY	721	ACAACTTTTACAAAGGACCAAGACGTTTGTATATCAATGGCAACGATATTGGAGTCGAC	780
Db	721	ACAACTTTTACAAAGGACCAAGACGTTTGTATATCAATGGCAACGATATTGGAGTCGAC	780
QY	781	TATTTAGAGGTCAAATATTCTATCAACCGGTGCTGTGACACCTCTTTTCCACCT	840
Db	781	TATTTAGAGGTCAAATATTCTATCAACCGGTGCTGTGACACCTCTTTTCCACCT	840

Db	781	TATTTAGAGGTCAAATATTCTATCAACCGGTGCTGTGACACCTCTTTTCCACCT	840
QY	841	TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGCTATCATCTATGTTCTTGAA	900
Db	841	TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGCTATCATCTATGTTCTTGAA	900
QY	901	GTAGCCAAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA	960
Db	901	GTAGCCAAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA	960
QY	961	ACGAAAACATTAAGTTACTTGGCCGGGTTTCATATCAATGACGACGCTGCTACTTCCGAT	1020
Db	961	ACGAAAACATTAAGTTACTTGGCCGGGTTTCATATCAATGACGACGCTGCTACTTCCGAT	1020
QY	1021	TTCTTGAACCGTGTACATGTCGAAGAAAATAAACTCAGATCTTTGGGATATGGAACCTT	1080
Db	1021	TTCTTGAACCGTGTACATGTCGAAGAAAATAAACTCAGATCTTTGGGATATGGAACCTT	1080
QY	1081	CCTCATCCTTGGCTTAACCTCTACGTTCTTAAATCTCGGATCTCGGATCTCTATCCCA	1140
Db	1081	CCTCATCCTTGGCTTAACCTCTACGTTCTTAAATCTCGGATCTCGGATCTCTATCCCA	1140
QY	1141	GTTGTCAAAGACATTTCTTAAAGCAAAATCAGCTTCGGGACTCGCTCTCTATCCA	1200
Db	1141	GTTGTCAAAGACATTTCTTAAAGCAAAATCAGCTTCGGGACTCGCTCTCTATCCA	1200
QY	1201	ACAAACCGGAATAAATGGGACAAATCGTATGTGCGGATGATACCAGAGATCGATGAAGAT	1260
Db	1201	ACAAACCGGAATAAATGGGACAAATCGTATGTGCGGATGATACCAGAGATCGATGAAGAT	1260
QY	1261	GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAGTGGAG	1320
Db	1261	GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAGTGGAG	1320
QY	1321	AGCGTTAACGAGAAAGATAATTAGGTTTTCGCAAGGATTCAGGTATTAGATTAAAGCAATAT	1380
Db	1321	AGCGTTAACGAGAAAGATAATTAGGTTTTCGCAAGGATTCAGGTATTAGATTAAAGCAATAT	1380
QY	1381	CTAATGCATTATACCTAGTAAAGAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT	1440
Db	1381	CTAATGCATTATACCTAGTAAAGAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT	1440
QY	1441	TTTTCGAAGAGGAAAGATCTATTGATCCCAAGAACTGTTATCTCCAGGCGCAAGACATC	1500
Db	1441	TTTTCGAAGAGGAAAGATCTATTGATCCCAAGAACTGTTATCTCCAGGCGCAAGACATC	1500
QY	1501	TTTTGA 1506	
Db	1501	TTTTGA 1506	

RESULT 2
ACC85294
ID ACC85294 standard; cDNA; 1506 BP.
XX

ACC85294;
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 2 cDNA.
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
XX embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX Arabidopsis thaliana.
XX
PN WO2003050287-A2.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP013990.
XX
PR 10-DEC-2001; 2001US-00014101.

XX (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX
PI Schmullling T, Werner T;
XX
DR WPI; 2003-541577/51.
XX
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.
XX
PS Claim 3; Page 167-168; 177pp; English.
XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
XX shown in the invention
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;
Query Match 100.0%; Score 1506; DB 8; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGGCTAATCTTCGTTTAATGATCATCTTTAATCAGCGTTTAAATGATCACCACCAATCATCA 60
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DB 61 AACGGTATTAAATTTGATTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC 120
QY 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACAATAACCCACCGTGACCCCGCGGCGTA 180
DB 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACAATAACCCACCGTGACCCCGCGGCGTA 180
QY 181 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCCTCCAATACGCCGCAACCGGAAAA 240
DB 181 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCCTCCAATACGCCGCAACCGGAAAA 240
QY 241 AGTACATCCAAAGTAGCGGCTCGTGCCCAAGGCCACTCTCTAAACGGCCAAAGCCTCGGTC 300
DB 241 AGTACATCCAAAGTAGCGGCTCGTGCCCAAGGCCACTCTCTAAACGGCCAAAGCCTCGGTC 300
QY 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAGACAAG 360
DB 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAGACAAG 360
QY 361 AAGTACGTGACGTGGCGGCCGCGGACGTTATGGGTGGATGTCTTAAGAAGACGCGGAG 420
DB 361 AAGTACGTGACGTGGCGGCCGCGGACGTTATGGGTGGATGTCTTAAGAAGACGCGGAG 420
QY 421 AAAGGGGTGTCGCCGGTTTCTTTGACGGATTATTTGCATATAACCGTCGGAGGAACGTTG 480
DB 421 AAAGGGGTGTCGCCGGTTTCTTTGACGGATTATTTGCATATAACCGTCGGAGGAACGTTG 480
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DB 481 TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACCGTCTCTTGTAGTAACGTCCTT 540
QY 541 GAATTGGACGTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCA 600
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DB 601 GAATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAATATAACGAGAGCCAGA 660
QY 661 ATTGTTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTATTC 720
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DB 721 ACAACTTTTACAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGAC 780
QY 781 TATTTAGAAGGTCAAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTTTCCACCT 840
DB 781 TATTTAGAAGGTCAAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTTTCCACCT 840
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DB 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACCGGTATCATCTATGTTCTTGA 900
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DB 901 GTAGCCAAAGTATTATGATGCCAATCTCCCATCATCAGCAAGGTATTGACACATTA 960
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DB 961 ACGAAACATTAAGTTACTTGTCCCGGTTTCAATCAATGCACGACGTGCTACTTCGAT 1020
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DB 1081 CCTCATCCTTGGCTTAACTTACCTTACGTTTCTTAATCTCGGATTCTCGATTTTTCATAACGGT 1140
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DB 1141 GTTGTCAAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCA 1200
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DB 1261 GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAGAGTGGAG 1320
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DB 1441 TTTTCGAAGAGGAAAGATCTATTGTATCCCAAGAAACTGTTATCTCCAGGGCAAGACATC 1500
QY 1501 TTTTGA 1506
DB 1501 TTTTGA 1506
RESULT 3
AAC43214
ID AAC43214 standard; DNA; 1548 BP.
XX
AC AAC43214;
XX

Db 541 GAATTGGACGTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCA 600
QY 601 GAATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAATATAACGAGAGCCAGA 660
Db 601 GAATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAATATAACGAGAGCCAGA 660
QY 661 ATTGTTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTATTC 720
Db 661 ATTGTTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTATTC 720
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Db 721 ACAACTTTTACAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGAC 780
QY 781 TATTTAGAAGGTCAAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTTTCCACCT 840
Db 781 TATTTAGAAGGTCAAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTTTCCACCT 840
QY 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACCGGTATCATCTATGTTCTTGA 900
Db 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACCGGTATCATCTATGTTCTTGA 900
QY 901 GTAGCCAAAGTATTATGATGCCAATCTCCCATCATCAGCAAGGTATTGACACATTA 960
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Db 1021 TTCTTGAAACCGTGTACATGTGGAAGAAATAAATACTCAGATCTTTGGGATTATGGAACTT 1080
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Db 1141 GTTGTCAAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCA 1200
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QY 1261 GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAGAGTGGAG 1320
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Db 1321 AGCGTTAACGAGAAAGATAATTAGGTTTTCGAAGGATTCAGGTATTAAGATTAAAGCAATAT 1380
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Db 1441 TTTTCGAAGAGGAAAGATCTATTGTATCCCAAGAAACTGTTATCTCCAGGGCAAGACATC 1500
QY 1501 TTTTGA 1506
Db 1501 TTTTGA 1506
RESULT 3
AAC43214
ID AAC43214 standard; DNA; 1548 BP.
XX
AC AAC43214;
XX

DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 38443.
DE
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS
XX
XX
PN EP1033405-A2.
XX
PD
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
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QY	61	AACGGTATTAAAATTGATTTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC 120
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QY	421	AAAGGGGTGTCGCCCGGTTTCTTGGACGGATTATTGATATAAACCGTCGGAGAACGTTG 480
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QY	601	GAATTGTTCTATGGAGTGTTAGGAGGTTGGGTCAATTTGGAATTATAACGAGGCCAGA 660
Db	601	GAATTGTTCTATGGAGTGTTAGGAGGTTGGGTCAATTTGGAATTATAACGAGGCCAGA 660
QY	661	ATTGTTTTTGGACCATGCACCTAAACCGGCGCAAAATGGTTTCGGATGCTCTACAGTATTC 720
Db	661	ATTGTTTTTGGACCATGCACCTAAACCGGCGCAAAATGGTTTCGGATGCTCTACAGTATTC 720
QY	721	ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAAAACGATATTGGAGTCGAC 780
Db	721	ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAAAACGATATTGGAGTCGAC 780
QY	781	TATTTAGAAGGTCAAATATTTCTATCAAACGGTGTGTTGACACCTCTTTTCCACCT 840
Db	781	TATTTAGAAGGTCAAATATTTCTATCAAACGGTGTGTTGACACCTCTTTTCCACCT 840
QY	841	TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACCGGTATCATCTATGTTCTTGAA 900
Db	841	TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACCGGTATCATCTATGTTCTTGAA 900
QY	901	GTAGCCAAAGTATTATGATGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTA 960
Db	901	GTAGCCAAAGTATTATGATGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTA 960
QY	961	ACGAAAACATTAAAGTTACTTGGCCGGGTTTCATATCAATGCACGACGTGSCCTACTTCGAT 1020
Db	961	ACGAAAACATTAAAGTTACTTGGCCGGGTTTCATATCAATGCACGACGTGSCCTACTTCGAT 1020
QY	1021	TTCTTGAACCGTGATCATGTGGAAGAAAATAAACTCAGATCTTTGGGATTATGGAACTT 1080
Db	1021	TTCTTGAACCGTGATCATGTGGAAGAAAATAAACTCAGATCTTTGGGATTATGGAACTT 1080
QY	1081	CCTCATCCTTGGCTTAACTCTACGTTCCCTAAATCTCGGATTCCTCGATTTTCATAACGGT 1140
Db	1081	CCTCATCCTTGGCTTAACTCTACGTTCCCTAAATCTCGGATTCCTCGATTTTCATAACGGT 1140
QY	1141	GTTGTCAAAGACATTCTTCTTAAGCAAAAATCAGTTCTGGGACTCGCTCTTCTATCCA 1200
Db	1141	GTTGTCAAAGACATTCTTCTTAAGCAAAAATCAGTTCTGGGACTCGCTCTTCTATCCA 1200
QY	1201	ACAAACCGGAAT-----AAATGG 1218
Db	1201	ACAAACCGGAATAAGTACATACTTCTTTCATTATTTATCTTCAAGAACCAAAATGG 1260
QY	1219	GACAAATCGTATGTGGCGGATGATACCAAGATCGATGAAAGATGTTATATATATTCGGA 1278
Db	1261	GACAAATCGTATGTGGCGGATGATACCAAGATCGATGAAAGATGTTATATATATTCGGA 1320
QY	1279	CTACTACAATCCGCTACCCCAAAGGATCTTCCAGAAAGTGGAGCGGTTAACGAGAAGATA 1338
Db	1321	CTACTACAATCCGCTACCCCAAAGGATCTTCCAGAAAGTGGAGCGGTTAACGAGAAGATA 1380

QY 1339 ATTAGGTTTTCGAAGGATTCAGGTATTAGATTAAAGCAATATCTAATGCATTATCTAGT 1398
 Db 1381 ATTAGGTTTTCGAAGGATTCAGGTATTAGATTAAAGCAATATCTAATGCATTATCTAGT 1440
 QY 1399 AAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTCGAAGAGGAAAGAT 1458
 Db 1441 AAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTCGAAGAGGAAAGAT 1500
 QY 1459 CTATTGATCCCAAGAACTGTTATCTCCAGGGCAAGACATCTTTGA 1506
 Db 1501 CTATTGATCCCAAGAACTGTTATCTCCAGGGCAAGACATCTTTGA 1548

RESULT 4

AAC42983

ID AAC42983 standard; DNA; 1575 BP.

AC AAC42983;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37588.

XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PN 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
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 PR 16-APR-1999; 99US-0129845P.
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 PR 23-APR-1999; 99US-0130510P.
 PR 28-APR-1999; 99US-0131449P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 51.7%; Score 778.2; DB 3; Length 1575;
Best Local Similarity 72.2%; Pred. No. 1.9e-228;

Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;
QY 42 AATGATCACCAAAATCATCAAACGGTATTAAAAATTGATTTACCTAAATCCCTTAACCTCAC 101
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Db 63 AACCTTAATCAAAATCAGATGAGGGCATTGATGTTTTCTTACCCATATCACTCAACCTTAC 122

QY 102 CCTCTCTACCGATCCTTCCATCATCTCCGACGCCTCTCATGACTTCGGAACATAACAC 161
|||
Db 123 GGTCTTAACCGATCCCTTCTCCATCTCTCGCGCTTCTCACGACTTCGGTAACATAACCGA 182

QY 162 CGTGACCCCGCGCGCGTAATCTGCCCCCTCTCCACCGCTGATATCTCTCGTCTCCTCC- 220
|||
Db 183 CGAAAATCCCGCGCGCTCCTCTGCCCCCTCTCCACCGAGGAGGTGCTCTCCTCCG 242

QY 221 -----AATACGCGCGCAACCGGAAAAAGTACATTCCA 251
|||
Db 243 TTTCGCTAACGGAGGATTCTCTTACAATAAAGGCTCAACGAGCCCCGCTCTACTTTCAA 302

QY 252 AGTAGCGGCTCGTGCCCAAGGCCACTCCTTAAACGGCCAAAGCCTCGGTCTCGGCGGAGT 311
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Db 303 AGTGGTCTCGAGGCCAAGGCCACTCCCTCCGTGGCCAAAGCCTCTGCACCCGGAGGTGT 362

QY 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGTTCAAA 353
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Db 363 CGTCGTGAACATGACGTGTCTCGCCATGGCGGCTAAACCAGCGCGGTGTTATCTCGGC 422

QY 354 AGACAAAGAAATACGCTGACGTGGCGCGCGGACGTTATTTGGACGGATTATTTGCATATAACCGTCCGAGG 473
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Db 423 AGACGGGACTTACGCTGACGTGGCTGCCGGACCATGTGGTGGATGTTCTGAAGCGCGC 482

QY 414 GCGGAGAAAAGGGTGTGCCCGGTTCTTGGACGGATTATTTGCATATAACCGTCCGAGG 473
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Db 483 GGTGGATAGAGCGTCTGCCCGGTTACATGGACGGATTATTTGTATCTCAGCGTCCGCGG 542

QY 474 AACGTTGTGGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCCCTCTGTTAGTAA 533
|||
Db 543 GACGTTGTGGAACGCTGGAATCGGTGGTCAGACGTTTAGACACGGCCCTCAGATTAGTAA 602

QY 534 CGTCCTTGAATGGACGTTATTACTGGGAAAGTGAAATGTTGACATGCTCGCACAGCT 593
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Db 603 CGTTCATGAGCTTGACGTTATTACCGGAAAGGTGAAATGATGACTTGGCTCTCCAAAGTT 662

QY 594 AAACCCAGAAATGTTCTATGGAGTGTTAGGAGTTTGGGTCAATTTGGAATTATAACGAG 653
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Db 663 AAACCCAGAAATGTTCTATGGAGTTTTAGGAGTTTGGGTCAATTCGGTATTATAACGAG 722

QY 654 AGCCAGAAATGTTTGGACCATGCACCTAAACGGGCGCAAAATGGTTTCGGATGCTCTACAG 713
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Db 723 GGCCAGGATTGCGTTGGATCATGCACCCACCAAGGGTGAAATGGTCTCGCATACTCTACAG 782

QY 714 TGATTTCAAACTTTTACAAAGSACCAAGAACGTTTGAATATCAATGGCAACGATATTGG 773
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Db 783 TGACTTCTCGGCTTTTAAAGAGAGACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGG 842

QY 774 AGTCGACTATTTAGAAGGTCAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTT 833
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Db 843 AGTTGACTTTTGGAAAGGTCAACTTATGATGTCAAATGGCTTCGTAGACACCTCTTTCTT 902

QY 834 CCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGT 893
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Db 903 CCCACTCTCCGATCAACAAGAGTCGCATCTCTTGTGAATGACCAACCGGATCATCTATGT 962

QY 894 TCTTGAAGTAGCCAAAGTATTATGATGATCCCCAATCTCCCCATCATCAGCAAGGTTATTGA 953
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Db 963 TCTCGAAGTAGCCAAAGTATTATGACAGAACCCCTTCCCATTATTGACCAGGTGATTGA 1022

QY 954 CACATTAACGAAAAACATTAAAGTTACTTTCGCGGGTTCATATCAATGACGACGCTGGCCTA 1013
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Db 1023 CACGTTAAGTAGAACTCTAGGTTTCGCTCCAGGGTTTATGTTGTTACAAAGATGTTCCGTA 1082

QY 1014 CTTGATTTTCTTGAACCGGTGTACATGTGGAAGAAAAATAAATCAGATCTTTGGGATTATG 1073
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Db 1083 TTTTCGATTTTCTTGAACCGGTGTCGGAACGGAAGAGATAAACTCAGATCTTTAGGACTATG 1142

QY 1074 GGAAGTTCCTATCCTTGGCTTAACCTTACGTTTCTTAATCTCGGATCTCGATTTTCA 1133
Db 1143 GGAAGTTCCTATCCTCATGGCTTAACATCTTGTCCGGGTCCTCGAATCCAAGATTTTCA 1202
QY 1134 TAACGGTGTGTCAAAGACATCTTCTTAAGCAAAAATCAGTTCGGGACTCGCTCTTCT 1193
Db 1203 TGATGGTGTATTAATGGCTTCTTCTAAACCAACCTCAACTTCTGGTGTACTCTCTT 1262
QY 1194 CTATCCAAACAAACCGGAATAAATGGGACATCGTATGTGCGGCGATGATACCAAGATCGA 1253
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QY 1254 TGAAGATGTTATATATATATATCGGACTACTACAATCCGC---TACCCCAAAAGGATCTTCC 1310
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QY 1311 AGAAGTGGAGAGCGTTAAACGAGAAGATAATTAGGTTTTTGCAGGATTCAGGTATTAAAGAT 1370
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QY 1371 TAAGCAATATCTAATGCAATATATACTAGTAAGAAGATTTGGATTGAGCATTTTGGATCAAA 1430
Db 1437 TAAGGAATATTTGATGCACATATACAAGAAAAGAAAGATTTGGTTAAACATTTTGGACCAA 1496
QY 1431 ATGGGATGATTTTTCGAAGAGGAAAAGATCTATTTGATCCCAAGAACTGTTATCTCCAGG 1490
Db 1497 ATGGGATGATTTTTTAAGAAAAGAAAATTTATGTTTGATCCCAAAAGACTATTGTCTCCAGG 1556
QY 1491 GCAAGACATCTTT 1503
Db 1557 ACAAGACATATTT 1569

RESULT 5
ABZ14284
ID ABZ14284 standard; DNA; 1575 BP.
XX AC ABZ14284;
XX DT 21-JAN-2003 (first entry)
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2089.
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX OS Arabidopsis thaliana.
XX PN WO200216655-A2.
XX PD 28-FEB-2002.
XX PF 24-AUG-2001; 2001WO-US026685.
XX PR 24-AUG-2000; 2000US-0227866P.
XX PR 26-JAN-2001; 2001US-0264647P.
XX PR 22-JUN-2001; 2001US-0300111P.
XX PA (SCRI) SCRIPPS RES INST.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Harper JF, Kreps J, Wang X, Zhu T;
XX DR WPI; 2002-304127/34.
XX PT Identifying a stress condition to which a plant cell has been exposed and
XX PT producing plants with increased tolerance to these abiotic stresses.
XX PS Claim 144; SEQ ID NO 2089; 577pp + Sequence Listing; English.
XX PS The invention relates to identifying a stress condition to which a plant
XX CC cell has been exposed, comprising: (a) contacting nucleic acid
XX CC representative of expressed polynucleotides in the plant cell with an

CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Query Match 51.7%; Score 778.2; DB 6; Length 1575;
Best Local Similarity 72.2%; Pred. No. 1.9e-228;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;
QY 42 AATGATCACCAAAATCATCAACGGTATTAAATTTGATTTACCTAAATCCCTTAACCTCAC 101
Db 63 AACCTTAATCAATCAGATGAGGCAATTGATGTTTCTTACCCATATCACTCAACCTTAC 122
QY 102 CCTCTCTACCGATCCTTCCATCATCTCCGAGCCTCTCATGACTTCGAAACATAACCAC 161
Db 123 GGTCCTAACCGATCCCTTCTCCATCTCTGCCGTTCTCACGACTTCGTAACATAACCGA 182
QY 162 CGTGACCCCGCGGGGTAATCTGCCCTCTCCACCGCTGATATCTCTGTCCTCTCC- 220
Db 183 CGAAATCCCGCGCGCTCTCTGCCCTTCTCCACCAACGAGGTTGGTCTCTCTCCG 242
QY 221 -----AATACGCCGCAACCGGAAAAAGTACATTCCA 251
Db 243 TTTCGCTAACGGAGGATTTCTTACAATAAAGGCTCAACCGCCCGCTACTTTCAA 302
QY 252 AGTAGCGGCTCGTGCCAAAGGCCACTCTTAAACGGCCAAAGCCTCGGTCCTCCGGCGAGT 311
Db 303 AGTGGCTGCTCGAGGCCAAAGGCCACTCCCTCCGTGGCCAAAGCCTCTGCACCCGGAGGT 362
QY 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA 353
Db 363 CGTCGTGAACATGACGTGTCTGCCATGGCGGCTAAACCGCGGTTGTATCTCGGC 422
QY 354 AGACAAGAAGTACGCTGACGTGGCGGGGACGTTATGGGTGGATGTGCTTAAGAAGAC 413
Db 423 AGACGGGACTTACGCTGACGTGGCTGCCGGACGATGTGGGTGGATGTTCTGAAGGCGGC 482
QY 414 GCGGAGAAAAGGGTGTCCCGGTTTCTTGGACGGATTTTGCATATAACCGTCGGGAGG 473
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QY 474 AACGTTGTGGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAA 533
Db 543 GACGTTGTGAAACGCTGGAATCGGTGGTCAGACGTTTAGACACGGCCCTCAGATTAGTAA 602
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Db 903 CCCACTCTCCGATCAAAACAGAGTCGCATCTCTGTGAATGACACCGGATCATCTATGT 962
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QY 1491 GCAAGACATCTTT 1503
Db 1557 ACAAGACATATTT 1569

RESULT 6
ABK28627
ID ABK28627 standard; cDNA; 1575 BP.

XX ABK28627;

AC 09-APR-2002 (first entry)

XX cDNA encoding A. thaliana cytokinin oxidase AtCKX4.

DE Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
XX root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarpy; gene; ss.

XX Arabidopsis thaliana.

OS WO200196580-A2.

XX 20-DEC-2001.

XX 18-JUN-2001; 2001WO-EP006833.

XX 16-JUN-2000; 2000EP-00870132.

XX 27-DEC-2000; 2000US-0258415P.

PR 16-MAR-2001; 2001EP-00870053.

XX (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.
XX Schmulling T, Werner T;
XX WPI; 2002-130736/17.
DR Polynucleotide encoding novel plant protein having cytokinin oxidase
XX activity and the protein useful for stimulating root growth, enhancing
PT the formation of lateral or adventitious roots, altering root geotropism.
PT Claim 2; Page 147-148; 154pp; English.
XX The invention relates to an isolated polynucleotide (I) encoding a novel
PS plant protein (II) having cytokinin oxidase activity. (I) is useful for
XX production of transgenic plants, plant cells or tissues; for production
CC of altered plants, plant cell or tissues; and for effecting the
CC expression of (II) where (I) is operably linked to one or more control
CC sequences. The methods further comprises regenerating a plant from the
CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarpy; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;
SQ Query Match 51.7%; Score 778.2; DB 6; Length 1575;
Best Local Similarity 72.2%; Pred. No. 1.9e-228;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;

QY 42 AATGATCACCAATCATCAACGGTATTAAATGATTACCTAAATCCCTTAACCTCAC 101
Db 63 AACCTTAATCAATCAGATGAGGCGATTGATGTTTCTTACCCTATATCACTCAACCTTAC 122
QY 102 CCTCTCTACCGATCCTTCATCATCTCCGACGCTCTCATGACTTCGGAACAATAACCAC 161
Db 123 GGTCTTAACCGATCCCTTCTCCATCTCTGCCGCTTCTCACGACTTCGGTAACATAACCGA 182
QY 162 CGTGACCCCGCGCGGCGTAATCTGCCCTCTCCACCGCTGATATCTCTGCTCCTCTCC- 220
Db 183 CGAAATATCCCGCGCGCTCTCTGCCCTTCTCCACCAACGAGGTGGTCTGCTCTCTCCG 242
QY 221 -----AATACGCGCGCAACGGAAGTACATTCCA 251
Db 243 TTTTCGTAAACGGAGGATTCTTACAATAAAGGCTCAACAGCCCCCGCTCTACTTTCAA 302
QY 252 AGTAGCGGCTCGTGCCCAAGGCCACTCTTAAACGCGCAAGCCTCGGTCTCCGGCGGAGT 311
Db 303 AGTGGCTGCTCGAGGCCAAGGCCACTCCCTCCGTGGCCAAAGCCTCTGCACCCGAGGTGT 362
QY 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA 353
Db 363 CGTCGTGAACATGACGTGTCTGCCCATGGCGGCTAAACAGCGGCGTGTATTCTCGGC 422
QY 354 AGACAAGAAGTACGCTGACGTGGCGGCGGACGTTATGGTGGATGTGCTTAAGAAGAC 413
Db 423 AGACGGGACTTACGCTGACGTGGCTGCCGGGACGATGGGTGGATGTTCTGAAGSGCGC 482
QY 414 GCGGAGAAAGGGGTGTCCCGGTTTCTTGGACGGATTATTTGCATATAACCGTCGGAGG 473
Db 483 GGTGGATAGAGCGGTCTCGCCGGTTACATGGACGGATTATTTGTATCTCAGCGTCGGCG 542
QY 474 AACGTTGTGCAATGGTGGAAATTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTATTAGTAA 533

Db 543 GACGTTGTCGAACGCTGGAATCGGTGTCAGACGTTTACACACGGCCCTCAGATTAGTAA 602
 QY 534 CGTCCTTGAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCT 593
 Db 603 CATTGATGAGCTTGACGTTATTACCGGAAAGGTGAAATGATGATGCTCTCCAAAGTT 662
 QY 594 AAAACCCAGAAATTGTTCTATGGAGTGTGAGAGGTTGGTCAATTGGAATTATAACGAG 653
 Db 663 AAAACCTGAATTGTTCTATGGAGTGTGAGAGGTTGGTCAATTGGAATTATAACGAG 722
 QY 654 AGCCAGAAATTGTTTGGACCATGACCTAAACGGGCCAAATGTTTGGATGCTCTACAG 713
 Db 723 GGCCAGGATTGGCTTGGATCATGACCCACAGGGTGAATGTTCTGCATATCTCTACAG 782
 QY 714 TGATTTACAACTTTTACAAAGGACCAAGAACGTTTGTATATCAATGGCAACGATATTGG 773
 Db 783 TGACTTCTCGGCTTTTAAAGAGACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGG 842
 QY 774 AGTCGACTATTAGAGGTCAAATATTTCTATCAACCGGTGCTGTGACACCTCTTTT 833
 Db 843 AGTTGACTTTTGGAGGTCAACTTATGATGTCAAATGGCTTCTGTAGACACCTCTTTCTT 902
 QY 834 CCCACCTTCAGATCAATCTAAAGTCGCTGATGTCAGTCAAGCAACACGGTATCATCTATGT 893
 Db 903 CCCACTCTCGATCAACAAAGAGTCGATCTCTTGTGAATGACACCGGATCATCTATGT 962
 QY 894 TCTGAAGTAGCCAAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGA 953
 Db 963 TCTCGAAGTAGCCAAAGTATTATGACAGAACCAACCTCTCCCATTTATGACAGGTTATGA 1022
 QY 954 CACATTAACGAAACATTAAGTTACTTGGCCCGGTTTCAATCAATGACGACGCTGGCTA 1013
 Db 1023 CACGTTAAGTAGAATCTAGGTTTCTGCTCCAGGTTTATGTTCTGACAGATGTTCCGTA 1082
 QY 1014 CTTGATTTCTTGAACCGGTGTACATGTCGAGAAATAAATACTCAGATCTTTGGGATTATG 1073
 Db 1083 TTTGATTTCTTGAACCGGTGTCCGAAACGAGAAAGATAACTCAGATCTTTAGGACTATG 1142
 QY 1074 GGAACCTTCTCATCTTGGCTTAACCTCTAGTCTTAAATCTCGATTTCTCGATTTCATCA 1133
 Db 1143 GGAAGTCTCTCATCTTGGCTTAACATCTTGTCCCGGGTCTCGAATCCAGATTTCATCA 1202
 QY 1134 TAACGGTGTGTCAAGACATTTCTTCTTAAGCAAAATCAGCTTCGGGACTCGCTCTCT 1193
 Db 1203 TGATGGTGTATTATAGGCTTCTTCTAAACCAACCTCAACITTTGTTACTCTCTT 1262
 QY 1194 CTATCCAAACAAACCGGAAATAAATGGGACAAATCGTATGTCGGCGATGATACCAGATCGA 1253
 Db 1263 CTATCCCAACAAACCGGAAATAAATGGGACAAATCGTATGTCGGCGATGATACCAGATCGA 1316
 QY 1254 TGAAGATGTTATATATATATATCGGACTACTACAATCCGC---TACCCCAAGGATCTTCC 1310
 Db 1317 CGAAGATGTTTATGATGATCGGATTACTGCAATCAGCTGGTGGATCTCAAAATTGSCA 1376
 QY 1311 AGAAGTGGAGAGCGTTTAAACGAGAGATATAGGTTTTCAGAGGATTCAGGTATTAAAGAT 1370
 Db 1377 AGAAGTGGAGAGCGTTTAAACGAGAGATATAGGTTTTCAGAGGATTCAGGTATTAAAGAT 1436
 QY 1371 TAAGCAATATCTAATGCAATTATCTAGTAAAGAGATTTGGATTGAGCATTTTGGATCAAA 1430
 Db 1437 TAAGCAATATTTGATGCACTATACAGAAAGAGATTTGGTTAAACATTTTGGACCAAA 1496
 QY 1431 ATGGGATGATTTTTCGAGAGAGGAAAGATCTATTGATCCCAAGAACTGTTATCTCCAGG 1490
 Db 1497 ATGGGATGATTTTTCGAGAGAGGAAATTTATGTTGATCCCAAGAACTGTTATCTCCAGG 1556
 QY 1491 GCAAGACATCTTT 1503
 Db 1557 ACAAGACATATTT 1569

RESULT 7

ADA68648
 ID ADA68648 standard; DNA; 1575 BP.
 XX
 AC ADA68648;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Arabidopsis thaliana gene, SEQ ID 428.
 XX
 KW Plant; bacterial infection; fungal infection; viral infection; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO2003000898-A1.
 XX
 PD 03-JAN-2003.
 XX
 PF 22-JUN-2001; 2001WO-IB001105.
 XX
 PR 22-JUN-2001; 2001WO-IB001105.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX
 DR WPI; 2003-175290/17.
 XX
 XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX
 PS Claim 6; SEQ ID NO 428; 899pp; English.
 XX
 CC The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX
 SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Query Match 51.7%; Score 778.2; DB 7; Length 1575;
 Best Local Similarity 72.2%; Pred. No. 1.9e-228;
 Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;
 QY 42 AATGATCACAAATCATCAACGGTATTAAATGATTACCTAAATCCCTTAACCTCAC 101
 Db 63 AACCTTAATCAATCAGATGAGGGCATTTGATGTTTCTTACCCATATCACTCAACCTTAC 122
 QY 102 CCTCTTACCGATCCTTCCATCATCTCCGAGGCTCTCATGACTTCGGAACATAACCCAC 161
 Db 123 GGTCTTAACCGATCCCTTCTCCATCTCTGCGGCTTCTCAGACTTCGGTAAACATAACCGA 182
 QY 162 CGTGACCCCGGCGGCGTAAATCTGCCCCCTCCCTCCACCGCTGATATCTCTCTCTCC- 220
 Db 183 CGAAATCCCGGCGGCGTCTCTGCCCCCTTCTCTCCACCGAGGCTGCTCTCTCCG 242
 QY 221 -----AATACGCGCAACCGAAAGGCTCAACGCCCCGGCTTACTTTCAA 251
 Db 243 TTTTCGTAACGGAGGATTCTCTTACAATAAAGGCTCAACGCCCCGGCTTACTTTCAA 302
 QY 252 AGTAGCGGCTCGTGGCCAGGCGCACTCTTAAACGGCCCAAGCCTCGGTCTCCGGCGAGT 311
 Db 303 AGTGGCTGCTCGAGGCGCAAGGCGCACTCCCTCGGTGGCCCAAGCCTCTGACCCGGAGGTGT 362
 QY 312 AATCGTCAAATGACGTGTATC-----ACTGACGTGGTGGTTTCAA 353

Db 363 CGTCGTGAACATGACGCTGCTGCCATGGCGGCTAAACACGCGCGGTGTTATCTCGGC 422
 QY 354 AGACAAGAAGTACGCTGACGTCGCGCGCGGACGCTATGCGGTGATGCTGTTAAGAAGAC 413
 Db 423 AGACGGGACTTACGCTGACGTCGCGGACGATGCTGGTGGATGTTCTGAAGCGGC 482
 QY 414 GCGCGAGAAAGGGGTGTCGCGGCTTCTTGGACCGGATTTTGCATATACCGTCGGAGG 473
 Db 483 GGTGGATAGAGCGCTCTCGCGGTTACATGGACGGATTTTGTATCTCAGCTCGCGG 542
 QY 474 AACGTTCTGGAATGGTGAATGGTGGTCAAGTGTTCGAAACGGTCTCTCTGTAGTAA 533
 Db 543 GACGTTGCGAACGCTGGAATCGGTGCTCAGACGTTTACACACGCGCCCTCAGATTAGTAA 602
 QY 534 CGTCCCTTGAATGGACGCTTATTACTGGGAAAGGTGAATGTTGACATGCTCGCGACAGCT 593
 Db 603 CGTTCATGAGCTTGACGCTTATTACCGGAAAGGTGAATGATGACTTGCTCTCAAAGTT 662
 QY 594 AAACCCAGAAATGTTCTATGGAGTGTAGGAGGTTTGGTCAATTTGGAAATTAACGAG 653
 Db 663 AAACCCGTGAATGTTCTATGGAGTGTAGGAGGTTTGGTCAATTCGGTATATTAACGAG 722
 QY 654 AGCCAGAAATGTTTGGACCAATGACACCTAAACGGGCGCAATGTTTCGGGATGCTCTACAG 713
 Db 723 GGCCAGGATGCGTGGATCAATGACCCCAAGGGTGAATGTTCTCGCATACTCTACAG 782
 QY 714 TGATTTTCAACAACTTTTACAAAGGACCAAGACGTTTGTATATCAATGGCAACGATATTGG 773
 Db 783 TGACTTCTCGGCTTTTAAAGAGAGACCAAGAGCGTTTATATATCAATGACCAATGATCTCGG 842
 QY 774 AGTCGACTATTAGAAAGGTCAAAATTTCTATCAACCGGTGTCGTTGACACCTCTTTT 833
 Db 843 AGTTGACTTTTGGAAAGGTCAACTATGATGTCAATGGGTTCTGTAGACACCTCTTTCTT 902
 QY 834 CCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGT 893
 Db 903 CCCACTCTCCGATCAACAAGAGTCGATCTCTTGTGATGACCAACCGGATCATCTATGT 962
 QY 894 TCTTGAAGTAGCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGA 953
 Db 963 TCTCGAAGTAGCAAGTATTATGACAGAACCAACCTTCCCATATTATGACCAAGGTTATGA 1022
 QY 954 CACATTAACGAAACATTAAGTTACTTCCCGGTTTCATATCAATGACGACGTCGCTTA 1013
 Db 1023 CACGTTAAGTAGAATCTAGGTTTCGCTCCAGGTTTATGTTGATCAAGATGTTCCGTA 1082
 QY 1014 CTTGATTTCTTGAACCGGTGATCATGTCGAAGAAATAAATCAATCATCAGATCTTTGGATATG 1073
 Db 1083 TTTGATTTCTTGAACCGGTGTCGAAGAAAGAAAGATAAATCAATCATCTTTAGGACTATG 1142
 QY 1074 GGAATTCCTCATCTTGGCTTAACCTTACCTTACCTTCTTAAATCTCGGATTCGATTTCA 1133
 Db 1143 GGAATTCCTCATCTTGGCTTAACATCTTGTCCCGGGTCTCGAATCCAAGATTTCA 1202
 QY 1134 TAACGGTGTGTCBAAGACATTTCTTCTTAAGCAAAATCAGCTTCGGGACTCGCTCTTCT 1193
 Db 1203 TGATGGTGTATTATAGGCTTCTTCTTAACCAACCTCAACTTCTGGTGTACTCTT 1262
 QY 1194 CTATCCAAACACCGGAATAAATGGGACAAATCGTATGTCGGCGATGATACGAGATCGA 1253
 Db 1263 CTATCCCAACACCGGAATAAATGGAAACACCGCATGTCAACGATGACACC-----GGA 1316
 QY 1254 TGAAGATGTTATATATATTATCGGACTACTACAAATCCGC---TACCCCAAGGATCTTCC 1310
 Db 1317 CGAAGATGTTTATATGATCGGATTAATGATCAATCAGCTGGTGGATCTCAAAATGGCA 1376
 QY 1311 AGAAGTGGAGAGCGTTAAACGAGAGATAATTAGGTTTTCGAAGGATTCAGGTATTAAAGAT 1370
 Db 1377 AGAAGTGGAAATCTCAACGACAGAGTTTATTCAGTTTGTGAAACCTCGGAATTAAGAT 1436
 QY 1371 TAAGCAATATCTAATGCAATTATCTAGTAAAGAGATTTGGATTGAGCATTTTGGATCAAA 1430

Db 1437 TAAGGAATATTGATGCACTATATACAGAAAGAGATTGGGTTAAACATTTTGGACCAA 1496
 QY 1431 ATGGGATGATTTTGAAGAGAGAAAGATCTATTTGATCCCAAGAAACTGTTATCTCCAGG 1490
 Db 1497 ATGGGATGATTTTGAAGAAAGAAATATGTTTATCCCAAAAGACTATTGTTCTCCAGG 1556
 QY 1491 GCAAGACATCTTT 1503
 Db 1557 ACAAGACATATT 1569
 RESULT 8
 ACC85296
 ID ACC85296 standard; cDNA; 1575 BP.
 XX
 AC ACC85296;
 XX
 DT 18-SEP-2003 (first entry)
 XX
 DE Arabidopsis cytokinin oxidase-like protein 4 cDNA.
 XX
 KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
 KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO2003050287-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2002; 2002WO-EP013990.
 XX
 PR 10-DEC-2001; 2001US-00014101.
 XX
 PA (SCHM/) SCHMULLING T.
 PA (WERN/) WERNER T.
 PI Schmulling T, Werner T;
 XX
 DR WPI; 2003-541577/51.
 XX
 PT Stimulating root growth, enhancing lateral or adventitious root formation
 PT or altering root geotropism comprises increasing plant cytokinin oxidase
 PT levels or other protein or nucleic acid that reduces active cytokinins in
 PT a plant.
 XX
 PS Claim 2; Page 169-170; 177pp; English.
 XX
 CC The present invention relates to a method for stimulating root growth or
 CC enhancing the formation of lateral or adventitious roots or altering root
 CC geotropism, which comprises increasing in a plant or plant part the level
 CC of a plant cytokinin oxidase or other protein that reduces the level of
 CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
 CC coding sequences from Arabidopsis thaliana are also provided. The method
 CC is useful in modifying plant morphological, biochemical and physiological
 CC properties, such as in modifying the initiation, stimulation or
 CC enhancement of root growth, adventitious root formation, lateral root
 CC formation, root geotropism, shoot growth, apical dominance, branching,
 CC timing of senescence, timing of flowering, flower formation, seed
 CC development and/or seed yield. The present sequence is a coding sequence
 CC shown in the invention
 XX
 SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;
 Query Match 51.7%; Score 778.2; DB 8; Length 1575;
 Best Local Similarity 72.2%; Pred. No. 1.9e-228;
 Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;
 QY 42 AATGATCACCACCAATCATCAACGGTATTAAATTTACCTAAATCCCTTAACCTCAC 101
 Db 63 AACCTTAATCAATCAGATGAGGGCATTTGTTTCTTACCATATCACTCAACCTTAC 122
 QY 102 CCTCTCTACCGATCCTTCCATCATCTCCGACGCTCTCATGACTTCGGAACATAACCAC 161

CC plant cell. (I) and (II) are useful for stimulating root growth;
CC enhancing the formation of lateral or adventitious roots; altering root
CC geotropism, leading to an increase in yield; and for screening growth
CC promoting chemical of herbicides. (I) is useful for increasing the size
CC of the root meristem; increasing root size; increasing the size of the
CC shoot meristem; delaying leaf senescence and altering leaf senescence;
CC increasing leaf thickness; reducing or increasing the vessel size;
CC inducing parthenocarp; improving standability of the seedlings;
CC increasing branching and for improving lodging resistance. Antibody (III)
CC to (II) is useful for identifying and obtaining proteins interacting with
CC (II) comprising a screening assay, preferably a two-hybrid screening
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase
CC coding sequences and PCR primers of the invention
XX
SQ Sequence 2991 BP; 920 A; 522 C; 521 G; 1028 T; 0 U; 0 Other;

Query Match 38.3%; Score 577; DB 6; Length 2991;
Best Local Similarity 75.9%; Pred. No. 2.5e-166;
Matches 852; Conservative 0; Mismatches 40; Indels 231; Gaps 2;

QY 615 AGTGTAGGAGGTTTGGGTCAATTGGAAATTATACAGAGAGCCAGAAATGTTTGGACCA 674
DB 1869 ACTGTAATATGTTTCTTTATATATGTTGTAATAAATGGAATGTTTCTCTCTAAA 1928
QY 675 TGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTATTTTCACAACCTTTACAAA 734
DB 1929 TGAATGTGTAGGCCAAATGGTTTCGGATGCTCTACAGTATTTTCACAACCTTTACAAA 1988
QY 735 GGACCAAGAACGTTTGTATATCAATATGGAACGATATTTGGAGTCGACTATTTAGAAGGTCA 794
DB 1989 GGACCAAGAACGTTTGTATATCAATATGGAACGATATTTGGAGTCGACTATTTAGAAGGTCA 2048
QY 795 AATATTTCTATCAAAACGGTGTCTGTTGACACCTCTTTTTCACCTTCAGATCAATCTAA 854
DB 2049 AATATTTCTATCAAAACGGTGTCTGTTGACACCTCTTTTTCACCTTCAGATCAATCTAA 2108
QY 855 AGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCCAACTATTA 914
DB 2109 AGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCCAACTATTA 2168
QY 915 TGATGATCCCAATCTCCCCATCATCAGCA----- 943
DB 2169 TGATGATCCCAATCTCCCCATCATCAGCAAGGTACTACAACTTACATTTTTCATCATCGT 2228
QY 944 ----- 943
DB 2229 TTTTATCATACCATAAAGATATTTTAAATGATTCATCATTTGCACACATTAAGATATTCATC 2288
QY 944 -----AGG 946
DB 2289 ATCATCATCGTTACATTTTTTTGGCATCTTATGCTTCTCTCAATCTACTATTGTGTAGG 2348
QY 947 TTATTGACACATTAACGAAACATTAAGTTACTTTGCCCGGGTTTCATATCAATGCACGACG 1006
DB 2349 TTATTGACACATTAACGAAACATTAAGTTACTTTGCCCGGGTTTCATATCAATGCACGACG 2408
QY 1007 TGGCCTACTTCGATTTCTTGAACCGTGTACATGTGGAAGAAATAAACTCAGATCTTTGG 1066
DB 2409 TGGCCTACTTCGATTTCTTGAACCGTGTACATGTGGAAGAAATAAACTCAGATCTTTGG 2468
QY 1067 GATTATGGGAACCTTCCTCATCCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTCCTG 1126
DB 2469 GATTATGGGAACCTTCCTCATCCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTCCTG 2528
QY 1127 ATTTTCATAACGGGTGTTGTCAAAGACATTTCTTTAAGCAAAATCAGCTTCGGGACTCG 1186
DB 2529 ATTTTCATAACGGGTGTTGTCAAAGACATTTCTTTAAGCAAAATCAGCTTCGGGACTCG 2588
QY 1187 CTCTTCTCTATCCAAACACCGGAATAA----- 1214
DB 2589 CTCTTCTCTATCCAAACACCGGAATAAGTACATACCTTCTCTTCATTCATATTATCTTC 2648
QY 1215 -----ATGGGACAA 1223

DB 2649 AAGAACCAAGTAATAAATTTCTATGAACGTGATTATGCTGTTATTGTTAGATGGACAA 2708
QY 1224 TCGTATGTCGGCGATGATACAGAGATCGATGAAGATGTTATATATATTATCGGACTACT 1283
DB 2709 TCGTATGTCGGCGATGATACAGAGATCGATGAAGATGTTATATATATTATCGGACTACT 2768
QY 1284 ACAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAGAGCGTTAAACGAGAGATAATTAG 1343
DB 2769 ACAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAGAGCGTTAAACGAGAGATAATTAG 2828
QY 1344 GTTTGCAAGGATTTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATAGTAAAGA 1403
DB 2829 GTTTGCAAGGATTTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATAGTAAAGA 2888
QY 1404 AGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATT 1463
DB 2889 AGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATT 2948
QY 1464 TGATCCCAAGAACTGTTATCTCTCCAGGGCAAGACATCTTTTGA 1506
DB 2949 TGATCCCAAGAACTGTTATCTCTCCAGGGCAAGACATCTTTTGA 2991

RESULT 10
ACC85276
ID ACC85276 standard; DNA; 2991 BP.

XX ACC85276;
AC 18-SEP-2003 (first entry)
DT Arabidopsis cytokinin oxidase-like protein 2 gene.
DE Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ds.
KW Arabidopsis thaliana.

OS WC2003050287-A2.
XX 19-JUN-2003.
PD 10-DEC-2002; 2002WO-EP013990.
PF 10-DEC-2001; 2001US-00014101.
PR (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.

XX Schmulling T, Werner T;
PI WPI; 2003-541577/51.
XX P-PSDB; ABR63569.

PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.

XX Claim 3; Page 145-146; 177pp; English.

PS The present invention relates to a method for stimulating root growth or
XX enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed

Query Match	31.2%;	Score 470;	DB 6;	Length 1572;
Best Local Similarity	58.7%;	Pred. No. 1.6e-133;		
Matches 881;	Conservative	0;	Mismatches 600;	Indels 21; Gaps 3;
QY	17	TAATGATCACTTTAATCAACGGTTTTTAATGATCAACAAATCATCAAAACGGTATTAAAAATTG	76	
DB	56	TCATCATTAATCTCTCAACTCCGATCACAACCAACATCACCAACCAATGGAATATCC	115	
QY	77	ATTACCTAAATCCCTTAACCTCAACCTCTCTACCGATCCTTCATCATCTCCGACGCT	136	
DB	116	TTTCACACAACGAATTGCGCGGAAACTCACCTCCTCCTCCCTCCGTCGAATCAGCCG	175	
QY	137	CTCATGACTTCGAAACATAAACCCGCGTACCCCGGCGGCGGTAATCTGCCCTCCTCCA	196	
DB	176	CCACAGATTCGGCCACGTACCAAAAATCTTCCCTTCGCGCGTCTTAATCCCTTCCG	235	
QY	197	CCGCTGATATCTCTCGTCTCTCCATACGCGCGCAAAACGGAAGTAATCCAAAGTAG	256	
DB	236	TTGAAGACATCACAGATCTCATAAAACCTCTTTTGACTCTCAACTGTCTTTTCCCTTAG	295	
QY	257	CGGCTCGTGGCCAAAGCCACTCTCTTAAACGGCCAAAGCCTCGGTCGCGGCGGAGTAATCG	316	
DB	296	CCGCTCGTGTACGGACACAGCCACCGTGGCCAAAGCCTCGGCTAAGACGGAGTTGTGG	355	
QY	317	TCAACATGACGTGTATCACTGACGTGG-----TGGTTTCAAAAAGACAAGAAAT	364	
DB	356	TCAACATGCGGTCCATGGTAAACCGGGATCGAGGTATCAAGGTGTCTAGGACCTGTTTAT	415	
QY	365	ACGCTGACGTGGCGGCGGGACGTTATGGTGGATGTGCTTAAAGAACGGCGGAGAAAG	424	
DB	416	ATGTTGACGTGGACGCTCGTGGCTATGGATGAGGTGTTGAATAAACTTTGGAGTTAG	475	
QY	425	GGGTGTCCCGGTTCTTGGACGGATTATTTGCATATAAACCGTCGGAGGAACGTTGTCTGA	484	
DB	476	GGTTAACGCCGGTTCTTGGACGGATTATTTGATTTAAACAGTCGGTGGACGTTATCAA	535	
QY	485	ATGGTGAATTCGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACGTCCTTGAAT	544	
DB	536	ACGGCGGAATTAGTGACAAACGTTTCGGTACGGTCCACAGATCACTAATGTTCTAGAGA	595	
QY	545	TGGACGTTATTACTGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCAGAAT	604	
DB	596	TGGATGTTATTACTGGAAAGGAGAGATTGCAACTGTTTCCAAGGACATGAACGCGATC	655	
QY	605	TGTTCTATGGAGTGTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGAATTG	664	
DB	656	TTTTCTTCGCGGTGTAGGAGGTTTGGGTCAATTCGGCATTATAACAAGAGCCAGAATTA	715	
QY	665	TTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTCAAA	724	
DB	716	AACTTGAAGTAGTCCGAAAGGGCCAAAGTGGTTAAGGTTTCTATACATAGATTCTCCG	775	
QY	725	CTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCT--GACT	781	
DB	776	AATTCAAGAGATCAAGAACGAGTGATATCGAAACGCGGTGTAGATTCTTAGAAG	835	
QY	782	ATTTAGAAGGTCAAATATTTCTATCAAAACGGTGTGGTGGACACCTCTTTTTTCCACCTT	841	
DB	836	GTTCCATTATGTTGGACCATGGCCCAACCGGATACTGGAGATCCACGTAATATCCACCGT	895	
QY	842	CAGATCAATCTAAAGTCGTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAG	901	
DB	896	CCGATCACTTGAGGATCGCCTCAATGGTCAACCGACATCGTGTCTACTGCTTGAAG	955	
QY	902	TAGCCAAAGTATTATGATGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTAA	961	
DB	956	TCGTCAAGTATTACGACGAAACTTCTCAATACACAGTCAACGAGGAAATGGAGAGTTAA	1015	
QY	962	CGAAACATTAAGTTACTTGGCCCGGTTTCATATCAATGACGACGCTGGCCTACTTCGATT	1021	
DB	1016	CGCATAGTTTAAACCATGTAAAGGGTTTATGTACGAGAAAGATGTACGTAATATGGAAT	1075	

QY	1022	TCTTGAACCGTGTACATGTTCGAAGAAAAATAAACTCAGATCTTTGGGATATATGGGAACCTTC	1081
Db	1076	TCCTAAACCGAGTTCGAACCGGAGAGCTAAACCTGAAATCCAAAGGCCAATGGGATGTTTC	1135
QY	1082	CTCATCCTTTGGCTTAACCTCTACGTTCCCTAAATCTCGGATCTCTCGATTTTCATAACCGGTG	1141
Db	1136	CACATCCATGGCTTAATCTCTTCGTACCAAAAACCTCAAATCTCCAAATTTGATGATGGTG	1195
QY	1142	TTGTCAAAGACATCTCTTCTTAAGCAAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCAA	1201
Db	1196	TTTTTAAGGGTATTATCTCTAAGAAATAACATCACTAGCGTCTCTGTTCTTGTTCCTATCCTA	1255
QY	1202	CAACCGGAATAAATGGGACAAATCGTATGTCGGCGATGATACCAGAGATCGATGAAGATG	1261
Db	1256	TGAATCGCAACAAGTGGAATGATCGGATGTCTGCCGCTATACCCGAG-----GAAGATG	1309
QY	1262	TTATATATATTATCGGACTACTACAATCCGCTACCCCAAAAGGATCTTCCAGAAGTGGAGA	1321
Db	1310	TATTTTATCGGTAGGGTTTTTAAGATCCGCGGGTTTGCACAATTGGGAGGCTTTTGATC	1369
QY	1322	CGGTTAACGAGAAGATAATTAGGTTTTTGCAAGGATTCAGGTATTAAAGATTAAAGCAATATC	1381
Db	1370	AAGAAACATGGAAATACTCAAGTTTTTGTGAGGATGCTAATATGGGGGTTATACAATATC	1429
QY	1382	TAATGCATTATACTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATT	1441
Db	1430	TTCCATTATCATTCATCACAGAAGGATGGGTTAGACATTTTGGTCCGAGGTGGAATATTT	1489
QY	1442	TTTCGAAGAGGAAAGATCTATTGTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCT	1501
Db	1490	TCGTAGAGAGAAAAATATAATATGATCCCAAAATGATATTATCACCGGGACAAAATATAT	1549
QY	1502	TT 1503	
Db	1550	TT 1551	
RESULT 12			
ACC85295			
ID	ACC85295 standard; cDNA; 1572 BP.		
XX			
AC	ACC85295;		
XX			
DT	18-SEP-2003 (first entry)		
XX			
DE	Arabidopsis cytokinin oxidase-like protein 3 cDNA.		
XX			
KW	Maize; root growth; root geotropism; cytokinin oxidase; seed size;		
KW	embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	WO2003050287-A2.		
XX			
PD	19-JUN-2003.		
XX			
PF	10-DEC-2002; 2002WO-EP013990.		
XX			
PR	10-DEC-2001; 2001US-00014101.		
XX			
PA	(SCHM/) SCHMULLING T.		
PA	(WERN/) WERNER T.		
XX			
PI	Schmulling T, Werner T;		
XX			
DR	WPI; 2003-541577/51.		
XX			
PT	Stimulating root growth, enhancing lateral or adventitious root formation		
PT	or altering root geotropism comprises increasing plant cytokinin oxidase		
PT	levels or other protein or nucleic acid that reduces active cytokinins in		
PT	a plant.		
XX			
PS	Claim 3; Page 168-169; 177pp; English.		

Claim 3; Page 168-169; 177pp; English.

XX The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a coding sequence
CC shown in the invention
XX

SQ Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;
Query Match 31.2%; Score 470; DB 8; Length 1572;
Best Local Similarity 58.7%; Pred. No. 1.6e-133;
Matches 881; Conservative 0; Mismatches 600; Indels 21; Gaps 3;

QY 17 TAATGATCACTTTAATCAACGGTTTAAATGATCACCACCAATCATCAACCGGTATTAAATG 76
DB 56 TCATCATTTACTCTCAACTCCGATCACAACCAACATCACCACCAACCATGGAATATCC 115
QY 77 ATTTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCCATCATCTCCGCGCCT 136
DB 116 TTTCACACACGAATTCGCCGGAATACTCACCTCTCTCTCTCTCGTCAATCAGCCG 175
QY 137 CTCATGACTTCGGAAACATAACCAACCGTACCCCGCGGCGTAATCTGCCCTCCTCCA 196
DB 176 CCACAGATTTCCGCCACGTCACCAAAATCTTCCCTTCCGCCGCTTAATCCCTTCC 235
QY 197 CCGTGATATCTCTCGTCTCCTCCAATACCGCGCAACCGGAAAGTACATTCCAAGTAG 256
DB 236 TTGAAGACATCAAGATCTCATAAACTCTTTTGACTCTCAACTGCTTTTCTTTAG 295
QY 257 CGGCTCGTGCCAAAGCCACTCTTAAACGGCCAAAGCCTCGGTCTCCGGCGGAGTAATCG 316
DB 296 CCGCTCGTGTTCACGACACAGCCACCGTGGCCAAAGCCTCGGCTAAAGACGGAGTTGG 355
QY 317 TCAACATGACGTGATCACTGACGTG-----TGGTTTCAAAGACAAAGAAGT 364
DB 356 TCAACATCGGTCCTATGGTAAACCGGATCGAGGTATCAAGTGTCTAGGACCTGTTAT 415
QY 365 ACGCTGACGTGGCGCGGACGTTATGGGTGATGCTTAAAGACACGGCGGAGAAAG 424
DB 416 ATGTTGACGTGGACGCTGCGTATGGATGAGGTGTTGAATAAAACTTTGGAGTTAG 475
QY 425 GGGTGTGCGCGGTTTCTTGGACGGATTATTTGCATATAACCGTCCGAGAAACGTTGTGA 484
DB 476 GGTAAACGCGGTTTCTTGGACGGATTATTTGTATTAACAGTCCGTTGGACGTTATCAA 535
QY 485 ATGTTGGAATTTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAAAGTCTCTTGAAT 544
DB 536 ACGCGGGAATTAGTGGACAAACGTTTCCGTAACGGTCCACAGATCACTAATGTTCTAGAG 595
QY 545 TGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCAGAAAT 604
DB 596 TGGATGTTATTACTGGAAGGAGAGATTGCAACTTGTTCGAAGGACATGAAGTCCGATC 655
QY 605 TGTCTATGAGTGTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGAAATTG 664
DB 656 TTTTCTTCGCGGTTTAGGAGGTTTGGGTCAATTCGGCATTAATAACAGAGCCAGAAATTA 715
QY 665 TTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGAFTTCACAA 724
DB 716 AACTTGAAGTAGTCCGAAAGGCGCAAGTGGTTAAGGTTTCTATACATAGATTTCTCCG 775
QY 725 CTTTTACAAAGGACCAAGACGTTTGATATCAATGGCAAACGATATTGGAGTC--GACT 781
DB 776 AATTCAAGAGATCAAGAACGAGTGATATCGAAACCGGCGGTGTAGATTTCTTAGAAG 835

QY 782 ATTTAGAAGGTCAAATATTTCTATCAAAACGGTGTGCTTGACACCTCTTTTCCACCTT 841
DB 836 GTTCCATTATGGTGACCATGCGCCACCGGATAAAGTGGAGATCCAGTATTATCCACCGT 895
QY 842 CAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTGAAG 901
DB 896 CCGATCACTTGAGGATCGCTCAATGGTCAAAACGACATCGTGTCTATCTACTGCTTGAAG 955
QY 902 TAGCCAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA 961
DB 956 TCGTCAAGTATTACGACGAACTTCTCAATACACAGTCAACGAGGAAATGGAGGATTA 1015
QY 962 CGAAACACATTAAGTTACTTGGCCGGTTCATATCAATGACACGACGTCCTACTTCGAT 1021
DB 1016 GCGATAGTTTAAACCATGTAAAGAGGTTTATGTACGAGAAAGATGTGACGTATATG 1075
QY 1022 TCTTGAACCGTGTACATGTGCAAGAAATAAACTCAGATCTTTGGGATTATGGGAATTC 1081
DB 1076 TCCTAAACCGAGTTCGAACCGGAGAGCTAAACCTGAAATCCAAAGGCCAATGGGATGTC 1135
QY 1082 CTCATCCTTGGCTTAACCTCTACGTTCTTAAATCTCGGATTTCTCGATTTTCTATAACGGTG 1141
DB 1136 CACATCCATGGCTTAATCTCTTCTGACCAAAACTCAATCTCCAAATTTGATGATGTTG 1195
QY 1142 TTGTCAAAGACATTTCTTTAAGCAAAATCAGCTTCGGGACTCGCTCTCTCTATCCAA 1201
DB 1196 TTTTAAAGGTATTATCTTAAGAAATAACATCAGTACGCGTCTGTTCTTGTATTATCCTA 1255
QY 1202 CAAACCGGAATAAATGGGACAATCGTATGTCCGCGATGATACAGAGATCGATGAAGATG 1261
DB 1256 TGAATCGCAACAGTGAATGATCGGATGTCTGCCGTATATACCCGAG-----GAAGATG 1309
QY 1262 TTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAGA 1321
DB 1310 TATTTTATGCGGTAGGTTTTTAAGATCCGCGGTTTTTGACAATTGGGAGGCTTTTGATC 1369
QY 1322 GCGTTAACGAGAAATATTAGGTTTTGCAAGGATTCAGGTATTAAAGATTAAGCAATATC 1381
DB 1370 AAGAAACATGGAATACTGAAGTTTTGTGAGGATGCTAATATGGGGTTATACATATC 1429
QY 1382 TAATGCATTATCTAGTAAAGAGATTGGATTGAGCATTTTGGATCBAATGGGATGATT 1441
DB 1430 TTTCTTATCATTCATCAAGAAAGGATGGGTAGACATTTTGGTCCGAGGTGGAATATT 1489
QY 1442 TTTTGAAGAGGAAAGATCTATTGATCCCAAGAACTGTTATCTCCAGGGCAAGACATCT 1501
DB 1490 TCGTAGAGAGAAATATAATATATGATCCCAAAATGATATTATCACCGGACAAATATAT 1549
QY 1502 TT 1503
DB 1550 TT 1551

RESULT 13
AAC36788
ID AAC36788 standard; DNA; 503 BP.
XX
AC AAC36788;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15080.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX

PF	25-FEB-2000;	2000EP-00301439.	
XX	25-FEB-1999;	99US-0121825P.	09-JUL-1999;
PR	05-MAR-1999;	99US-0123180P.	PR 12-JUL-1999;
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PR	20-JUL-1999;	99US-0144884P.	
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PR	31-AUG-1999;	99US-0151438P.	
PR	01-SEP-1999;	99US-0151930P.	
PR	07-SEP-1999;	99US-0152363P.	
PR	10-SEP-1999;	99US-0153070P.	
PR	13-SEP-1999;	99US-0153758P.	
PR	15-SEP-1999;	99US-0154018P.	
PR	16-SEP-1999;	99US-0154039P.	
PR	20-SEP-1999;	99US-0154779P.	
PR	22-SEP-1999;	99US-0155139P.	
PR	23-SEP-1999;	99US-0155486P.	
PR	24-SEP-1999;	99US-0155659P.	

PR 28-SEP-1999; 99US-0156458P.
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PR 04-OCT-1999; 99US-0157117P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 30.6%; Score 461.2; DB 3; Length 503;
Best Local Similarity 99.2%; Pred. No. 4.3e-131;
Matches 482; Conservative 2; Mismatches 0; Indels 2; Gaps 2;

QY 559 GGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCAGAAATGTTCTATGGAGTG 618
Db 18 GGGAAAGGTGAAATGTTGACATGCTCGGACAG-TAAACCCAGAAATGTTCTATGGAGTG 76
QY 619 TTAGGAGGTTGGGTCAATTTGGAATTATAACGAGAGCCAGAAATGTTTGGACCATGCA 678
Db 77 TTAGGAGGTTGGGTCAATTTGGAATTATAACGAGAGCCAGAAATGTTTGGACCATGCA 136
QY 679 CCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTCAAACTTTTACAAAGGAC 738
Db 137 CCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTCAAACTTTTACAAAGGAC 196
QY 739 CAAGAACGTTTGATATCAATGCGCAACGATATTGGAGTCGACTATTTTAGAAGGTCAAATA 798
Db 197 CAAGAACGTTTGATATCAATGCGCAACGATATTGGAGTCGACTATTTTAGAAGGTCAAATA 256
QY 799 TTTCTATCAAAACGGGTGTCGTTGACACCTCTTTTTCACCTTCAGATCAATCTAAAGTC 858
Db 257 TTTCTATCAAAACGGGTGTCGTTGACACCTCTTTTTCACCTTCAGATCAATCTAAAGTC 316
QY 859 GCTGATCTAGTCAAGCAACACGCGTATCATCTATGTTCTTGAAGTAGCCAAAGTATTAT-GA 917
Db 317 GCTGATCTAGTCAAGCAACACGCGTATCATCTATGTTCTTGAAGTAGCCAAAGTATTATGGA 376
QY 918 TGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTAAACGAAACATTAAAGTTA 977
Db 377 TGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTAAACGAAACATTAAAGTTA 436
QY 978 CTTGCCCGGGTTTATATCAATGCACGACGTGGCCTACTTCGATTCTTGAACCGGTGACA 1037
Db 437 CTTGCCCGGGTTTATATCAATGCACGACGTGGCCTACTTCGATTCTTGAACCGGTGACA 496

QY 1038 TGTCGA 1043
Db 497 TGTCGA 502
RESULT 14
AAX02919
ID AAX02919 standard; DNA; 1602 BP.
XX
AC AAX02919;
XX
DT 20-MAY-1999 (first entry)
XX
DE Z. mays ckl1 degenerate DNA.
XX
KW Cytokinin oxidase; ckl1; transgenic plant; altered growth behaviour;
KW cytokinin-associated pathogenesis; resistance; fungi; nematode; assay;
KW grain yield; secondary growth; metabolism; senescence; ss.
XX
OS Zea mays.
XX
PN WO9906571-A1.
XX
PD 11-FEB-1999.
XX
PF 30-JUL-1998; 98WO-US015844.
XX
PR 30-JUL-1997; 97US-0054268P.
PR 29-JUL-1998; 98US-00124541.
XX
PA (UMOR) UNIV MISSOURI.
XX
PI Morris RO;
XX
DR WPI; 1999-153800/13.
PT New cytokinin oxidase from maize - used to generate transgenic plants
PT with, e.g. better disease resistance and growth characteristics.
XX
PS Claim 7c; Page 130-131; 140pp; English.
XX
CC This sequence encodes a Zea mays cytokinin oxidase, ckl1. This gene is
CC used to generate transgenic plants in which cytokinin-associated
CC pathogenesis or growth behaviour is altered. Particularly applications
CC include generation of plants with increased resistance to fungi and
CC nematodes, increased grain yield and superior secondary growth
CC properties. Host cells are used for production of recombinant ckl1
CC nucleic acid which is useful in an assay for determining cytokinin
CC concentrations, and for its studying effects on plant growth and
CC metabolism, including senescence
XX
SQ Sequence 1602 BP; 211 A; 179 C; 336 G; 205 T; 0 U; 671 Other;

Query Match 21.2%; Score 318.6; DB 2; Length 1602;
Best Local Similarity 36.7%; Pred. No. 6.8e-87;
Matches 543; Conservative 230; Mismatches 636; Indels 72; Gaps 8;

QY 89 CCCTTAACCTCACCCCTCTCTACCGATCCTTCCATCATCTCCGAGCCTCTCATGACTCG 148
Db 125 CNYTNGAYGGNAARYTNMGACNGAYWSNAAYGCNACNGCNGCNGSNACNGAYTYG 184
QY 149 GAAACATAACACCGTGACCCCGCGCGGTAATCTGCCCTCTCCACCGCTGATATCT 208
Db 185 GNAAYATHACNWSNGCNYTNCNGCNGCNGTNYTNTAYCCNWSNACNGGNGAYTTNG 244
QY 209 CTCGTCTCTTCCAATACGC--CGCAACGGAAAGATACATTCGAAGTAGCGGCTCGT 265
Db 245 TNGCNYTNTNWSNGCNGCAAYWSNACNCCNGGNTGGCCNTAYACNATHGCTTYMNG 304
QY 266 GCCAAGGCGACTCCTTAAACGGCCAGCCTCGGTCTCCGGCGGAGTAATCGTCAACATGA 325
Db 305 GNMGNNGNCAYWSNYTNATGGGNCARGCNTTYGCNCCNGGNGGNGTNGTNGTNAAYATGG 364

Db	1439	TYTGIGAYYTNGCNGGNATHCARTAYAAACNTAYTYTNGCNMGNCAACNGAYMGNWSNG	1499
Qy	1406	ATTGGATTGAGCATTTTGGAT---CAAAATGGGATGATTTTTCGAGAGGAAAGATCTAT	1462
Db	1499	AYTGGGTNMGNCAYTTTYGGNGCNGCNAARTGGAAYMGNTTYGTNGARATGAARAAYAART	1558
Qy	1463	TTGATCCCAAGAAACTGTTATCTCCAGGCAAGACATCTTT	1503
Db	1559	AYGAYCCNAARMGNYTNYTWSNCCNGGNCARGAYATHTTY	1599
RESULT 15			
ABK28628			
ID	ABK28628	standard; cDNA; 1611 BP.	
XX	AC	ABK28628;	
XX	DT	09-APR-2002 (first entry)	
XX	DE	cDNA encoding A. thaliana cytokinin oxidase AtCKX5.	
XX	KW	Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;	
KW	KW	root growth; lateral root; adventitious root; root geotropism; herbicide;	
KW	KW	root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.	
XX	OS	Arabidopsis thaliana.	
XX	PN	WO200196580-A2.	
XX	PD	20-DEC-2001.	
XX	PF	18-JUN-2001; 2001WO-EP006833.	
XX	PR	16-JUN-2000; 2000EP-00870132.	
PR	PR	27-DEC-2000; 2000US-0258415P.	
PR	PR	16-MAR-2001; 2001EP-00870053.	
XX	PA	(SCHEM/) SCHMULLING T.	
PA	PA	(WERN/) WERNER T.	
XX	PI	Schmulling T, Werner T;	
XX	PI	WPI; 2002-130736/17.	
DR	XX	Polynucleotide encoding novel plant protein having cytokinin oxidase	
PT	PT	activity and the protein useful for stimulating root growth, enhancing	
PT	PT	the formation of lateral or adventitious roots, altering root geotropism.	
XX	XX	Claim 3; Page 148-149; 154pp; English.	
PS	XX	The invention relates to an isolated polynucleotide (I) encoding a novel	
CC	CC	plant protein (II) having cytokinin oxidase activity. (I) is useful for	
CC	CC	production of transgenic plants, plant cells or tissues; for production	
CC	CC	of altered plants, plant cell or tissues; and for effecting the	
CC	CC	expression of (II) where (I) is operably linked to one or more control	
CC	CC	sequences. The methods further comprises regenerating a plant from the	
CC	CC	plant cell. (I) and (II) are useful for stimulating root growth;	
CC	CC	enhancing the formation of lateral or adventitious roots; altering root	
CC	CC	geotropism, leading to an increase in yield; and for screening growth	
CC	CC	promoting chemical of herbicides. (I) is useful for increasing the size	
CC	CC	of the root meristem; increasing root size; increasing the size of the	
CC	CC	shoot meristem; delaying leaf senescence and altering leaf senescence;	
CC	CC	increasing leaf thickness; reducing or increasing the vessel size;	
CC	CC	inducing parthenocarp; improving standability of the seedlings;	
CC	CC	increasing branching and for improving lodging resistance. Antibody (III)	
CC	CC	to (II) is useful for identifying and obtaining proteins interacting with	
CC	CC	(II) comprising a screening assay, preferably a two-hybrid screening	
CC	CC	assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase	
CC	CC	coding sequences and PCR primers of the invention	
XX	XX	Sequence 1611 BP; 416 A; 379 C; 409 G; 407 T; 0 U; 0 Other:	
SQ			

Query Match	20.3%; Score 306.2; DB 6; Length 1611;
Best Local Similarity	53.6%; Pred. No. 4.5e-83;
Matches	775; Conservative 0; Mismatches 628; Indels 42; Gaps 5;
QY	95 ACCTCACCTCTCTACCGATCCTTCCATCATCTCCGACGCTCTCATGACTTCGGAACA 154
Db	
	110 ACGCCACTTCACCGTCCACCTCCGACTTAGCCTCCGTCTCCTCAGACTTCGGTATGC 169
QY	155 TAA---CCACCGTGACCCCGCGCGGTAACTGCCCCCTCTCCACCGCTGATATCTCTC 211
Db	
	170 TGAAGTCACCTGAAGAGCCATTGGCCGTGCTTCATCCATCATCGGCCGAAGACGTGGCAC 229
QY	212 GTCTCTCCAATACGCCGCAACCGAAAAAGTACATTCGAAGTAGCGGCTCGTGGCCAAG 271
Db	
	230 GACTCGTCAGAACAGCTTACGGTTCAGCCACGGCGTTCCGGTCTCAGCCCGAGGCCACG 289
QY	272 GCCACTCCTTAAACGGCCAAAGCCTCG-----GTCTCCGCCGAGTAATCG 316
Db	
	290 GCCATTCATAAACCGACAAGCCGCGCGGGAGAACGGTGTGGTGTGAAATGAATGAACC 349
QY	317 TCACATGACGTGTATCACTGACGTGGTGGTTCCTTAAAGAACGCGGAGAAAGGGGTGTCGCCGG 436
Db	
	410 GGGGTGAGAGTTATGGTTCGATGTGTGAAGAAAAAGTGGAGCATGGCTTAGCACCAA 469
QY	437 TTTCTTGACGGATTATTTGCATATAAACCGTCGGAGAACGTTGTCGAATGGTGAATTG 496
Db	
	470 AATCATGACGGATTACTTGTATCTAACCGTTGGAGGTACACTCTCCAATGCAGGAATCA 529
QY	497 GTGGTCAAGTGTTCGAAACGGTCCCTCTTGTAGTAACGTCCTTGAATTTGGACGTTATTA 556
Db	
	530 GTGGTCAAGCTTTTACCATGGTCTCAAATTAGTAACGTCCTTGAGCTCGACGTTGTAA 589
QY	557 CTGGAAAGGTGAAATGTTGACATGCTCCGACAGCTAAACCCAGAAATGTTCTATGGAG 616
Db	
	590 CTGGAAAGGAGAGGTGATGAGATGCTCAGAAGAGAGAACACAGGCTATTCATGGAG 649
QY	617 TGTTAGGAGTTGGGTCAAATTTGGAATTATAACGAGAGCCAGAAATGTTTGGACCATG 676
Db	
	650 TTCTTGGTGGATTAGGTCAAATTTGGGATCATCACTCGAGCAGCACTCTCTCGAACCCAG 709
QY	677 CACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTTCACAACTTTTACAAGG 736
Db	
	710 CTCCCCAAGGGTGAGATGGATACGGGTATGTATTTCGAGCTTCAAAGTGTTCAGGAGG 769
QY	737 ACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGACTATTAGAAGGTCAA 796
Db	
	770 ACCAAGAGTACTTAATCTCAATGTCATGGTCAAATTAAGTTTGAATTACGTGGAAGGTTTG 829
QY	797 TATTTCTATCAACGGTGTGTTGACA-----CCTCTTTTTTCCACCTTCAGATC 847
Db	
	830 TGATTGTGACGAAGGACTCGTCAACAAATGGAGATCTCTTTCTCTCTCCACGTAACC 889
QY	848 AATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCCA 907
Db	
	890 CCGTCAAGATCTCCTCTGTAGTTTCCAACGGCTCTGTTTGTATTGCCTTGAGATCACCA 949
QY	908 AGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTATTGACACATTAACGAAAA 967
Db	
	950 AGAACTACCAGACTCCGACTCCGAAATCGTTGATCAGGAAGTTGAGATTCGATGAAGA 1009
QY	968 CATTAAGTTACTTGCCCGGTTTCATATCAATGCACGAGTGGCCCTACTTCGATTTCTTGA 1027
Db	
	1010 AATTGAATTCATACCGACATCGGTCTTTACAACGGAATTAACAATATGTGGACTTTCTCG 1069
QY	1028 ACCGTGTACATGTGGAAGAAAAATAAATCAGATCTTTGGGATTTATGGGAATCTTCCTCATC 1087
Db	
	1070 ACCGGGTACACAAGGCCGAATTGAAGCTCCGGTCCAAGAAATTTATGGGAGTTCCACACC 1129
QY	1088 CTGGCTTAACCTCTACGTTCCCTAAATCTCGGATTCCTCGAATTTTCATAACGGTGTGTCA 1147

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OM nucleic - nucleic search, using sw model

Run on: April 6, 2004, 20:47:22 ; Search time 4231 Seconds
(without alignments)
10629.271 Million cell updates/sec

Title: US-10-014-101-26
Perfect score: 1506
Sequence: 1 atggctaattcttggttaatt.....cagggaagacatcttttga 1506

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	31.9	561	AU236872	AU236872
2	368.8	24.5	689	CD813279	CD813279 BN15.019B
3	350.6	23.3	688	BZ006516	BZ006516 oeg06a08.
4	324.4	21.5	838	BH575041	BH575041 BOG8T82TR

C	5	290.2	19.3	436	9	AU227876
C	6	288.6	19.2	792	28	BZ078445
C	7	207.4	13.8	679	28	BZ030054
	8	203.6	13.5	626	14	CB9222686
C	9	200.8	13.3	683	28	BZ006156
	10	195.2	13.0	776	28	BZ500353
	11	188.8	12.5	553	10	AW623777
	12	188.6	12.5	510	14	CF607152
	13	186.8	12.4	601	13	BU025625
	14	185.2	12.3	451	13	BQ588342
	15	180.6	12.0	707	14	CD843876
	16	176.6	11.7	488	10	AW429072
C	17	174.2	11.6	401	9	AV810994
	18	171.4	11.4	566	13	BU084470
	19	169.8	11.3	635	10	BE330968
	20	168.4	11.2	811	14	CF439478
	21	168.2	11.2	582	12	BM143498
	22	162.8	10.8	550	29	CNS000MU
	23	161.6	10.7	641	28	BH007926
	24	160.4	10.7	779	28	BH513855
	25	150	10.0	560	29	CC958884
C	26	147.6	9.8	1016	28	BZ435515
	27	147.4	9.8	481	9	AV536711
	28	143.2	9.5	552	12	BM528151
	29	138.8	9.2	642	12	BI203744
	30	138.8	9.2	715	12	BI204708
	31	135.8	9.0	545	28	BH007927
	32	133.2	8.8	1776	11	AY112108
	33	130.8	8.7	407	13	BQ968442
C	34	130.8	8.7	699	28	BZ340096
	35	129.6	8.6	665	10	AW573644
	36	129	8.6	677	12	BI931101
	37	128.8	8.6	528	12	BG154047
C	38	128.8	8.6	617	13	BQ871609
	39	127.4	8.5	769	12	BG582720
	40	125	8.3	809	14	CF209921
	41	124.8	8.3	525	12	BI498566
	42	124.2	8.2	505	12	BI927011
	43	123.2	8.2	631	9	AV835311
	44	123	8.2	312	13	BQ916347
	45	123	8.2	854	28	BH722055

ALIGNMENTS

RESULT 1
AU236872

LOCUS
DEFINITION

AU236872 561 bp mRNA linear EST 01-APR-2002
AU236872 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-29-H04 5',
mRNA sequence.

ACCESSION
VERSION

AU236872
AU236872.1 GI:19876041

KEYWORDS
SOURCE

EST.
Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS

1 (bases 1 to 561)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J.,
Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A.,
Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)

TITLE
JOURNAL

Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp

COMMENT

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES
source
1. .561
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAF15-29-H04"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAF15"
/note="Site_1: BamHI; Site_2: SalI"

ORIGIN

Query Match 31.9%; Score 480; DB 9; Length 561;
Best Local Similarity 99.0%; Pred. No. 1.9e-121;
Matches 502; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 ATGGTAATCTTCGTTTAATGATCACTTTAATCACGGTTTAAATGATCACCAATCATCA 60
Db |||||
QY 61 AACGGTAAATAATGATTTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC 120
Db |||||
QY 115 AACGGTAAATAATGATTTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC 174
QY 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACATAAACACCGTGACCCCGGGCGGTA 180
Db |||||
QY 175 ATCATCTCCGAGCCTCTCATGACTTCGGAACATAAACACCGTGACCCCGGGCGGTA 234
QY 181 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCCTCAATACGCCGCAACCGAAAA 240
Db |||||
QY 235 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCCTCAATACGCCGCAACCGAAAA 294
QY 241 AGTACATTCAAAGTAGCGGCTCGTGCCCAAGGCCACTCCTTAAACGGCCAAAGCCTCGGTC 300
Db |||||
QY 295 AGTACATTCAAAGTAGCGGCTCGTGCCCAAGGCCACTCCTTAAACGGCCAAAGCCTCGGTC 354
QY 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGTGTTTCAAAAGACAAG 360
Db |||||
QY 361 AAGTACGCTGACGTGGCGGCGGACGTTATGGTGGATGTGCTTAAGAAGACGGCGGAG 420
Db |||||
QY 415 AAGTACGCTGACGTGGCGGCGGACGTTATGGTGGATGTGCTTAAGAAGACGGCGGAG 474
QY 421 AAAGGGGTGTCGCGGTTTCTTGGACGGATTATTGTCATATAA-CCGTGGAGGAACGTT 479
Db |||||
QY 475 AAAGGGGTGTCGCGGTTTCTTGGACGGATTATTGTCATATAACCCGTCGGANGAACGTT 534
QY 480 GTCGAATGGTGG-AATTGGTGGTCAAG 505
Db |||||
535 NTCNAATGGTGGAAATTGGTGGTCAAG 561

RESULT 2
CD813279 689 bp mRNA linear EST 10-JUL-2003
LOCUS BN15.019B17F020122 BN15 Brassica napus cDNA clone BN15019B17, mRNA
DEFINITION sequence.
ACCESSION CD813279
VERSION CD813279.1 GI:32495219
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 689)

AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.infobiogen.fr>.

FEATURES
source
1. .689
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN15019B17"
/tissue_type="seed"
/clone_lib="BN15"

ORIGIN

Query Match 24.5%; Score 368.8; DB 14; Length 689;
Best Local Similarity 80.2%; Pred. No. 1.3e-90;
Matches 465; Conservative 0; Mismatches 97; Indels 18; Gaps 2;

QY 1 ATGGCTAATCTTCGTTTAATGATCACTTTAATCACGGTTTAAATGA----- 46
Db |||||
QY 102 ATGGCTAATCTTCGTTTAATGATCACTTTAATCACGGTTTGGTTTATTTATTCGAGC 161
Db |||||
QY 47 -TCACCAATCATCAACCGGTATTA---ATTGATTACCTAAATCCCTTAACCTCACC 102
Db |||||
QY 162 TTTGTAAATCGTCAGAAAGCACTAAAGTTATTACTCTACCTAAAGTCCCTAAACCTCACC 221
QY 103 CTCTCTACCGATCCTTCCATCATCTCCGAGCCCTCTCATGACTTCGGAACATAACACACC 162
Db |||||
QY 222 CTCCTCACCGATCCTTCAACCATCTCCACCGCCTCTCACGATTACGGAAACGTTACACACC 281
QY 163 GTGACCCCGCGGGCGGTAATCTGCCCCCTCTCCACCGCTGATATCTCTCGTCTCCTCACA 222
Db |||||
QY 282 GTGACACCCCGCGGGCTCTCTGCGCTTCTCTCCCGCGAGATATTCGGTCTCCTACGC 341
QY 223 TACGCGCAACCGAAAGATACATTCGAAGTAGCGGCTCGTGGCCAAAGGCCACTCCTTA 282
Db |||||
QY 342 TACGCGCAACCGAGAGACTATATTCGAAGTGCGGCTCGAGCCAAAGGCCACTCTTTA 401
QY 283 AACGGCCAAAGCCTCGGTCTCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTG 342
Db |||||
QY 402 AACGGCCAAAGCCTCGGTATCAGGTGGAGTGGTTATCAACATGACGTGTCTCGTGACATA 461
QY 343 GTGGTTTCAAAGACAAGAGTACGCTGACGTGGCGGCCGGGACGTTATGGTGGATGTG 402
Db |||||
QY 462 ACTGTTTCAGAAACAAGAGTATGCTGACGTGGCAGGGCGGACGTTATGGTGGATGTG 521
QY 403 CTTAAGAAGACGCGGAGAAAGGGGTGTCGCCGGTTTCTTGGACGGATTATTGTCATATA 462
Db |||||
QY 522 CTTAGAGAGACGCGGAGCAAGGGCTTTCGCCGGTTTCGGGACGGATTATTGTCATATT 581
QY 463 ACCGTGGAGGAACGTTGTGGAATGGTGAATTGGTGGTCAAGTTCGAAACGGTCCCT 522
Db |||||
QY 582 AGCGTCGGAGGAACGCTGTGGAATGCTGGAATCGGCGGTCAAATGTTAGAAACGGTCCCT 641
QY 523 CTTGTTAGTAACGTCCTTGAATTGGACGTTATTACTGGGA 562
Db |||||
642 CAAATTAGTAACGTCCTTGAGTTGGACGTTATAACTGGTA 681

RESULT 3
BZ006516
LOCUS oeg06a08.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION sequence.

BZ006516 688 bp DNA linear GSS 07-OCT-2002
oeg06a08.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.

ACCESSION BZ006516
VERSION BZ006516.1 GI:23554774
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 688)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeg06 row: a column: 08
Seq primer: -28RppOT reverse
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
FEATURES Location/Qualifiers
1..688
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.Oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."
ORIGIN
Query Match 23.3%; Score 350.6; DB 28; Length 688;
Best Local Similarity 82.7%; Pred. No. 1.4e-85;
Matches 401; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 78 TTTACCTAAATCCCTTAACCTCAACCTCTCTACCGATCCTTCCATCATCTCCGAGCCTC 137
DB 29 TCTACCCAAATCGTTAAACCTCAACCTCTCTAACCAGATCCTTCCGCCATCTCCGCCCTC 88
QY 138 TCATGACTTCGGAACATAAACACCGTGACCGCCCGCGGCGTAATCTGCCCTCTCCAC 197
DB 89 TCACGATTTTGGAAACATCACTACCGTGATACCCGGTGGCGTGATCGCCCTTCTCTCTCC 148
QY 198 CGCTGATATCTCTCGTCTCCTCCAATACGCGCAAAACGGAAAAAGTACATTCGAAGTAGC 257
DB 149 CGCTGAGATATCCCGTCTCTCAGCTACGCTCTTAACGGAGAAAGAAAGTTCCAAGTGGC 208
QY 258 GGCTCGTGGCCAAAGGCCACTCCTTAAACGGCCAAAGCCTCGGTCCTCCGGCGGAGTAATCGT 317
DB 209 AGCTCGGGCCAAAGGCCACTCCTTGAAGGGTCAAGCAGCAGTCCTCAACGGAGTAATCGT 268
QY 318 CAACATGACGTGTATCACTGACGTGGTGGTTTCAAAAGACAAAGATACGCTGACGTGGC 377
DB 269 CAACATGACGTGTCTCGTGGCGTAGTGATTTTCAGATGACATGAAGTATGCTGACGTGGC 328
QY 378 GGCCGGGACGTTATGGGTGGATGTGCTTAAGAGACGGCGGAGAAAGGGGTGTGCGCCGGT 437
DB 329 CGGTGGGACGTTATGGGTGTGATGTGCTGAAAAAATACGGCGGAGAAAGGCGTTTCGCCGGT 388
QY 438 TTCTTGGACGGATTATTTCATATAACCGTCCGAGGAACGTTGTTCGAATGTGGAATTGG 497
DB 389 TTCTTGGACGGATTATTTCATGTTAGCATCGGAGGAACACTGTCAAAATGTGGAATCGG 448
QY 498 TGGTCAAGTGTTCGAAACGGTCTCTTGTGTAGTACGTCTCTTGAATTGGACGTTATTAC 557
DB 449 CGGTGAAGTGTTTAGAAACGGTCTCTCAGATTAGTAAAGTCTCTTGTGAGTTGGACGTTATAAC 508

QY 558 TGGGA 562
DB 509 TGGTA 513
RESULT 4
BH575041/c
LOCUS
DEFINITION BOG82TR BOGB Brassica oleracea genomic clone BOG82, genomic
survey sequence.
ACCESSION BH575041
VERSION BH575041.1 GI:17827114
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 838)
AUTHORS Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOG82TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES Location/Qualifiers
1..838
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BOG82"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN
Query Match 21.5%; Score 324.4; DB 28; Length 838;
Best Local Similarity 74.6%; Pred. No. 2.8e-78;
Matches 473; Conservative 0; Mismatches 81; Indels 80; Gaps 2;
QY 944 AGGTATTGACACATTAAACGAAACATTAAAGTACTTCCCGGTTTATCAATGCACG 1003
DB 640 AGGTATTGACAAAGTTAACTAAACCCCTAAGTTACTTCCCGGTTTATCAATGCACG 581
QY 1004 ACGTGGCCTACTTCGATTTCTTGAACCGTGATCATGTGAAAGAAATAAACTCAGATCTT 1063
DB 580 ACGTCTCTACTTTTGATTTCTCTGAACCGTGTAAGATTGAAGAGATAAACTCAGATCTC 521
QY 1064 TGGGATTATGGGAACCTTCCTCATCCTTGGCTTAAACCTCTACGTTCCCTAAATCTCGGATTC 1123
DB 520 TGGCTTTATGGGAAGTTCTCTCATCCATGGCTTAACTCTATGTCCCTAAACTCAGATAC 461
QY 1124 TCGATTTTCATAACGGTGTGTCAAAGACATTTCTTAAAGCAAAATCAGCTTCGGGAC 1183
DB 460 TAGATTTCCATAACGGTGTGTAAAGACATTTCTCTCAAGCAGAACTCGACTTCTGGCG 401
QY 1184 TCGCTCTTCTCTATCCAAACAAACCGGAATAA----- 1214
DB 400 TTGCTCTCTTCTATCCCAACCAACCGGAATAAGTAAGTTATTTCATACTAATCTTCAAGAA 341
QY 1215 -----ATGGGACAATCGTAT 1229
DB 340 CAAGTAACTAGATCTTGACATAATGTTTTTCTTGTTATTATTAGATGGGACAATGGTAT 281
QY 1230 GTCGGCGATGATACCAGAGATCGATGAAGATGTTTATATATATTATTCGGACTACTACAATC 1289

Db 280 GTCCGCGATGATACCA-----GATGAAGATGTTTCTATGTCGTGGGACTACTACAGGC 227
QY 1290 CGCTACCCCAAAGGATCTTCAGAAAGTGGAGAGCGTTAAACGAGAAGATAAATTAGGTTTTG 1349
Db 226 AGCTAGCTCACAAAATGTGCAAGAGTGGAGAGTGTAACCGAGCGCATATTAGGTTTTG 167
QY 1350 CAAGGATTCCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATATAGTAAAGAAAGATTG 1409
Db 166 CAAGGACTCGGGTATTAAAGATTAAAGCAGTATCTAATGCATTTTCACCGAAAAAGAAAGATTG 107
QY 1410 GATTGAGCATTTTGGATCAAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATTTGATCC 1469
Db 106 GGTGGAACATTTTGGATCTAAATGGGGTGCTTTTTCGAAGAGGAAAGATCTGTTTGATCC 47
QY 1470 CAAGAAACTGTTATCTCCAGGGCAAGACATCTTT 1503
Db 46 TAAGAACTATTATCTCCAGGGCAAGATATTTT 13

RESULT 5
AU227876/c
LOCUS AU227876 436 bp mRNA linear EST 23-APR-2002
DEFINITION AU227876 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-29-H04 3', mRNA sequence.
ACCESSION AU227876 GI:19742523
VERSION AU227876
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS 1 (bases 1 to 436)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekirtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sali. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES
source
1. .436
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-29-H04"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/note="Site_1: BamHI; Site_2: Sali"

ORIGIN
Query Match 19.3%; Score 290.2; DB 9; Length 436;
Best Local Similarity 95.1%; Pred. No. 6.1e-69;
Matches 311; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

QY 1180 GGACTCGCTCTCTCTATCCACAACCGGAATAAATGGGCAATCGTATGTCGGCGATG 1239
Db 431 GGACTCGCTGTTCTCTATCCACAACCGGAATAAATGGGCAATCTATGTC---GGCATG 375

QY 1240 ATACCAGAGATCGATGAAGATGTTTATATATATATATCGGACTACTACATCCGCTACCCCA 1299
Db 374 ATACCAGAGATCGATGAAGATGTTTATATATATATATCGGACTACTACATCCGCTACCCCA 315
QY 1300 AAGGATCTTCCAGAAGTGGAGAGCGTTAAACGAGAAGATAAATTAGGTTTTGCAAGGATTCA 1359
Db 314 AAGGATCTTCCAGAAGTGGAGAGCGTTAAACGAGAAGATAAATTAGGTTTTGCAAGGATTCA 255
QY 1360 GGTATTAAAGATTAAAGCAATATCTAATGCATTATATAGTAAAGAAAGATTGAGCAT 1419
Db 254 GGTATTAAAGATTAAAGCAATATCTAATGCATTATATAGTAAAGAAAGATTGAGCAT 195
QY 1420 TTTGGATCAAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATTTGATCCCAAGAAACTG 1479
Db 194 TTTGGATCAAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATTTGATCCCAAGAAACTG 135
QY 1480 TTATCTCCAGGGCAAGACATCTTTTGA 1506
Db 134 TTATCTCCAGGGCAAGACATCTTTTGA 108

RESULT 6
BZ078445/c
LOCUS BZ078445 792 bp DNA linear GSS 10-OCT-2002
DEFINITION BZ078445 11f25a09.g1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION BZ078445 GI:23702365
VERSION BZ078445
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS 1 (bases 1 to 792)
Delchaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole Genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: 11f25 row: a column: 09
Seq primer: -28RppOT reverse
Class: shotgun
High quality sequence start: 12
High quality sequence stop: 551.

FEATURES
source
1. .792
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN
Query Match 19.2%; Score 288.6; DB 28; Length 792;
Best Local Similarity 77.6%; Pred. No. 2.3e-68;
Matches 364; Conservative 0; Mismatches 99; Indels 6; Gaps 1;

QY 1 ATGGCTAATCTTCGTTTAAATGATCATCTTTAATCACGGTTTAA-----TGATCACCAA 54
Db 495 ATGGCTGATCTTCCTCTAATGATAACTCTAATGACGGTCTGTGATTTATTACTTCAAGC 436
QY 55 TCATCAACGGGTATTAAATTGATTACCTAAATCCCTTAACCTCACCTCTCTACCGAT 114

Db 435 TGTATCAATCGTCAGAGATTATTCTACCCAAATCGTTAAACCTCACCCCTCCTTAACCGAT 376
QY 115 CCTTCCATCATCTCCGAGCCTCTCATGACTTCGGAAACATAAACACCGTGACCCCGGC 174
Db 375 CCTTCCGCATCTCCGCGCCTCTCACGATTTTGGAAACATCACTACCGTGATACCGGT 316
QY 175 GCGTAATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCCTCAATACGCCGCAAAAC 234
Db 315 GCGGTGATCGCCCTTCTCTCCCGCTGAGATATCCCGTCTCCTCAGCTACGCCCTTAAC 256
QY 235 GGAAGATACATTCCAAGTAGCGGCTCGTGGCCAAAGGCCACTCCTTAAACGGCCAAAGCC 294
Db 255 GGAGAAAGAAAGTTCCAAGTGGCAGCTCGCGGCCAAAGGCCACTCCTTGAAGGGTCAAGCA 196
QY 295 TCGGTCTCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAA 354
Db 195 GCAGTCTCAACGGAGTAATCGTCAACATGACGTGTCTCGCTGGCGTAGTGTGATTCAGAT 136
QY 355 GACAAGATGACCTGACGTGGCGCGGACGTTATGGGTGATGTGCTTAAGAAGACG 414
Db 135 GACATGAAGTATGCTGACGTGGCGGTGGACGTTATGGGTGATGTGCTGAAAAATACG 76
QY 415 GCGGAGAAAGGGTGTCCCGGTTTCTTGGACGGATTATTTCATATAA 463
Db 75 GCGGAGAAAGCGGTTTCGCCGGTTTCTTGGACGGATTATTTCATGTTA 27
RESULT 7
BZ030054/c
LOCUS BZ030054 679 bp DNA linear GSS 08-OCT-2002
DEFINITION oeg01c05.g1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION BZ030054
VERSION BZ030054.1 GI:23599512
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS 1 (bases 1 to 679)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeg01 row: C column: 05
Seq primer: -28RppOT reverse
Class: shotgun
High quality sequence start: 8
High quality sequence stop: 551.
FEATURES
source Location/Qualifiers
1..679
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 13.8%; Score 207.4; DB 28; Length 679;
Best Local Similarity 84.1%; Pred. No. 6.4e-46;
Matches 248; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 1212 TAAATGGGACAATCGTATGTGCGCGATGATACCAGAGATCGATGAAGATGTTATATATAT 1271
Db 597 TAGATGGGACAATGGTATGTGCGCGATGATACCA-----GATGAAGATGTTTCTATGT 544
QY 1272 TATCGGACTACTACAATCCGCTACCCCAAAGGATCTTCCAGAAGTGGAGAGCGTTAACGA 1331
Db 543 CGTGGGACTACTACAGGCAGCTAGCTCACAAAATGTGCAAGAAAGTGGAGAGTGTAACGA 484
QY 1332 GAAGATAATTAGGTTTTCGAAGGATTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTA 1391
Db 483 GGCATCATTAGGTTTTCGAAGGACTCGGGTATTAAAGATTAAAGCAGTATCTAATGCATTT 424
QY 1392 TACTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAG 1451
Db 423 CACCAGAAAAGAAGATTGGTTGGAACATTTTGGATCTAAATGGGTCCTTTTTCGAAGAG 364
QY 1452 GAAAGATCTATTGTATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCTTTTGA 1506
Db 363 GAAAGATCTGTTGATCCTAAGAAACTATTATCTCCAGGGCAAGATATTTTGA 309
RESULT 8
CB922686
LOCUS CB922686 626 bp mRNA linear EST 25-APR-2003
DEFINITION VVD086G02 356005 An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera cDNA clone VVD086G02 5, mRNA sequence.
ACCESSION CB922686
VERSION CB922686.1 GI:30137348
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
AUTHORS 1 (bases 1 to 626)
Cushman,J.C.
TITLE An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay
JOURNAL Unpublished (2002)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 086 row: G column: 02
Seq primer: T3 20mer
High quality sequence stop: 626.
FEATURES
source Location/Qualifiers
1..626
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVD086G02"
/tissue_type="berries"
/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 13.5%; Score 203.6; DB 14; Length 626;
Best Local Similarity 62.8%; Pred. No. 7e-45;
Matches 355; Conservative 0; Mismatches 195; Indels 15; Gaps 2;
QY 364 TAGCTGACGTGGCGCGGACGTTATGGTGGTGTGCTTAAGAAGACGGCGAGAAA 423

Db 70 TATGCTGATCGGGGTGAGCAGCAATGGATTGATGTACTGCAAGCTACGCTCAACAT 129
QY 424 GGGGTGTCGGGTTTCTTGGACGGAATATTGTCATATAACCGTCGGAGGAACGTTGTG 483
Db 130 GGACTTGCACCAAGTGCCTGGACTGACTATTGTACCTAACCAATGGTGGTACACTCT 189
QY 484 AATGGTGAATGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACGTCCTTGA 543
Db 190 AATGCCGAATAGCGGCCAGACATTCGCCCATGGTCTCAGATCAGCAACGTCCTATGA 249
QY 544 TTGGACGTTTACTTACTGGAAAGGTGAATGTTGACATGCTCGGACAGCTAAACCCAGAA 603
Db 250 ATGGATGTTCTACTGTTAAAGGGAACTGTGACTTGTTCCAAAGACACAACTCTGAG 309
QY 604 TTGTTCTATGAGTGTTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGATT 663
Db 310 CTGTTTTTTCGGTCTTAGGAGGTCCTCGGCAGTTTGGGATTATAACAGAGCAAGGATC 369
QY 664 GTTTTGGACCATGCACCTAAACCGGCCCAATGTTTCGGATGCTCTACAGTGATTTCACA 723
Db 370 GCTCTAGAACCGGACCAGAAAGAGTAATGGATACAGATGCTTTACGATGACTTCTCC 429
QY 724 ACTTTTACAAAGGACCAAGAACGTTTGTATATCAATGGCAACCGATATTGGAGTCGACTAT 783
Db 430 ACATTTTCTAGAGACCAAGAACATTTGATTTCAAT-----CAATGGACTGGACTAT 480
QY 784 TTAGAAGGTCAATATTCTATCAACCGGTGCTGTTGACACC-----TCTTTTTTCCCA 837
Db 481 TTGGAAGGTTCACTCTCCATGCAAAATAGTCTCTTAATAACTGGAGATCCTCTTCTCA 540
QY 838 CTTTCAGATCAATCAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTT 897
Db 541 CCTCTGAATACCCGAGAAATATCTTCACTAATATCCAAAGATGGCATCATCTACTGCCTT 600
QY 898 GAAGTAGCCCAAGTATTATGATGATC 922
Db 601 NGAGTGGTCAAGTATTACGATGAAC 625

RESULT 9
BZ006156/c
LOCUS 683 bp DNA linear GSS 07-OCT-2002
DEFINITION oeg06a08.b1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION BZ006156
VERSION BZ006156.1 GI:23554414
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 683)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeg06 row: a column: 08
Seq primer: -21UPpOT forward
Class: shotgun
High quality sequence start: 32
High quality sequence stop: 551.
Location/Qualifiers
1. .683
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.Oleracea002"

/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
Query Match 13.3%; Score 200.8; DB 28; Length 683;
Best Local Similarity 84.3%; Pred.No. 4.3e-44;
Matches 226; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 680 CTAACCGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTTCAAACTTTTACAAAGGACC 739
Db 604 CTATGTAGGCGAAATGGTTTCGAATGCTGTACAGTCACTTTCACAGCTTTTACAAAGGACC 545
QY 740 AAGAACGTTTGTATATCAATGGCAACGATATTGGAGTCGACTATTAGAAAGGTCAAATAT 799
Db 544 AAGAACGTTTGTATATCAATGGCCGATGATGCTGGAGTTGATTATTAGAAAGGTCAAATAT 485
QY 800 TTCTATCAAAACGGTGTGTTGACACCTCTTTTCCACCTTCCAGCTTCAAGTCAATCTAAAGTCG 859
Db 484 TCATGTCAAAACGGGCTCGTAGACACCTCTTTTCCACAGTCAATCAATCTAAATATCG 425
QY 860 CTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCCAAAGTATTATGATG 919
Db 424 CTGATTTAGTGAAGAGCCACGGTATCATATATGTTCTTGAAGTAGCCAAAGTTTATTATGATG 365
QY 920 ATCCCAATCTCCCATCATCAGCAAGGT 947
Db 364 ATCCTACACTTCCCATCATTGGCCAGGT 337
RESULT 10
BZ500353
LOCUS 776 bp DNA linear GSS 16-DEC-2002
DEFINITION BONRD06TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONRD06, genomic survey sequence.
ACCESSION BZ500353
VERSION BZ500353.1 GI:27016257
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 776)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BONRD06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1. .776
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BONRD06"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHOS1; Site:1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 13.0%; Score 195.2; DB 28; Length 776;
Best Local Similarity 85.2%; Pred. No. 1.6e-42;
Matches 218; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 307 GGAGTAATCGTCAACATGACGCTGTATCACTGACGCTGGTGGTTTCAAAAGACACAAGTAC 366
|||||
Db 2 GGAGTGGTTATCAACATGACGCTGCCGCTGACATAACTGTTTCAGAAGACAAAGAGTAT 61
|||||

QY 367 GCTGACGTGGCGCGCGGACGTTATGGTGGATGTGCTTAAGAAGACGCGCGGAGAAAGGG 426
|||||
Db 62 GTTGACGTGGCGCGCGGACGTTATGGTGGATGTGCTTAGAGAGACGCGCGGAGAAAGGC 121
|||||

QY 427 GTGTGCGCGGTTCTTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTGTGCAAT 486
|||||
Db 122 GTTTCGCGGTTTCTTTGGACGGATTATTGTCATATTAGCGTCGGAGGAACGCTGTCTAAT 181
|||||

QY 487 GGTGGAATTGGTGGTCAAGTCTTTCGAAACGGTCCCTCTTGTAGTAACGTCCTTGAATTG 546
|||||
Db 182 GCTGGAATCGCGGTCAAGTGTTTAGAAACGGTCCCTCAAAATTAGTAACGTCCTTGAGTTG 241
|||||

QY 547 GACGTTATTACTGGGA 562
|||||
Db 242 GACGTTATAATTGGTA 257
|||||

RESULT 11
AW623777 553 bp mRNA linear EST 18-MAY-2001
LOCUS EST321722 tomato flower buds 3-8 mm, Cornell University
DEFINITION Lycopersicon esculentum cDNA clone cTOB1317 5', mRNA sequence.

AW623777

AW623777.1 GI:7336804

EST.

Lycopersicon esculentum (tomato)

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 553)

van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E.,

Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M.,

Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and

Tanksley,S.D.

Generation of ESTs from tomato flower tissue, 3-8 mm buds

Unpublished (1999)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1..553

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="cTOB1317"

/tissue_type="flower"

/dev_stage="3-8mm buds"

/clone_lib="tomato flower buds 3-8 mm, Cornell University"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; supplier: Tanksley; Flower buds and flowers were

taken from greenhouse plants (4-8 wks old, TA496). They

were immediately frozen in liquid nitrogen and then

size-separated while remaining frozen."

ORIGIN

Query Match 12.5%; Score 188.8; DB 10; Length 553;

Best Local Similarity 60.4%; Pred. No. 8.3e-41;

Matches 332; Conservative 0; Mismatches 212; Indels 6; Gaps 1;

QY 479 TGTCGAATCGTGGAAATTGGTGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACGTCC 538

Db 3 TCCTCTAATCGTGTATTTAGTGGTCAAAACTAACCGATATGGTCCGAAATAAGTAACGTAC 62
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QY 539 TTGAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACC 598
|||||
Db 63 ATGAGATGGATGTAATTACAGGTAAGGGGAATTAAATGACTTGCTCCAAAGATATGAATT 122
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QY 599 CAGAATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCA 658
|||||
Db 123 CAGAATTGTTTGGAGTTTTAGGAGGTTTGGGACAGTTTGGGAATAATAACAAGAGCAA 182
|||||
QY 659 GAATTGTTTGGACCATGCACCTTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATT 718
|||||
Db 183 GAATTGTTCTGGATAAAGCACCACCAAGAGTGAAATGGGTGAGAATGTTATATGATGATT 242
|||||
QY 719 TCACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGSCAAACGATATTGGAGTCG 778
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Db 243 TCTCAAAATTCACAAAGATCAAGAACATCTTATTCAATTCAATAATAAATGATGGATT 302
|||||
QY 779 ACTATTTAGAACGTCAAATATTTCTATCAAAACGGTGTGCTTGACA-----CCTCTTTT 832
|||||
Db 303 ATGTTGAAGGCTCTCTAATGATGGAGCAAGCTCTCTAAATAATTGGAGATCTTCAATTT 362
|||||
QY 833 TCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATG 892
|||||
Db 363 ATTCACCTTCCAATCAAAACCAAAATTTGCTTCATTATTATCCAAAATAAAATCATGTATT 422
|||||
QY 893 TTCTTGAAGTAGCCAAAGTATTATGATGATCCCCAATCTCCCCATCATCAGCAAGTTATTG 952
|||||
Db 423 GCTTGGAAATAGTGAAGTACTATGATGACCAAAATGCTAATACTATTGATAAGGAGTTGA 482
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QY 953 ACACATTAAACGAAACATTAAAGTTACTTGCCCGGGTTTCATATCAATGACGACGTTGGCCT 1012
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Db 483 AGAAGTTGGTAAAGGATTGAAGTATGTAGTGGATTATTGTTCAAGAAAGATGTGAGTT 542
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QY 1013 ACTTCGATTT 1022
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Db 543 TTGTGGAATT 552
|||||

RESULT 12

CF607152

LOCUS

DEFINITION

CF607152

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF607152 510 bp mRNA linear EST 30-SEP-2003
GEMMA01_000608 Grape Bud pSPORT1 Library Vitis vinifera cDNA 5',
mRNA sequence.

CF607152

CF607152.1 GI:37187799

EST.

Vitis vinifera

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; Vitaceae; Vitis.

1 (bases 1 to 510)

Moser,C., Segala,C., Pontana,P., Salakhudtinov,I., Gatto,P.,

Pindo,M., Zyprian,E., Toepfer,R., Grando,M.S. and Velasco,R.

Expressed sequence tags from different organs of Vitis vinifera

Unpublished (2003)

Contact: Moser C

Laboratorio di Genetica Molecolare

Istituto Agrario di San Michele all'Adige (IASMA)

via E. Mach 1, San Michele all'Adige (TN), I-38010, Italia

Tel: 0039-0461-615314

Fax: 0039-0461-650956

Email: claudio.moser@ismaa.it

The sequencing work has been funded by the 'Fondazione Cassa di

Risparmio di Trento e Rovereto'

High quality sequence stop: 510.

Location/Qualifiers

1..510

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Pinot noir"

FEATURES

source

/db_xref="taxon:29760"
/sex="Hermaphrodite"
/dev_stage="bud swelling"
/lab_host="DH10B"
/clone_lib="Grape Bud pSPORT1 Library"
/note="Organ: bud; Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 12.5%; Score 188.6; DB 14; Length 510;
Best Local Similarity 64.8%; Pred. No. 9e-41;
Matches 300; Conservative 0; Mismatches 154; Indels 9; Gaps 1;
QY 364 TACGCTGACGTGGCGGCCGACGCTTATGGTGGATGTGCTTAAGAAGACGGCGGAGAAA 423
Db 48 TATGCTGATCTGGGGGTGAGCAGCTATGGATTGATGTGCTGCAAGCTACGCTCAAAACAT 107
QY 424 GGGGTGTCGCCGGTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTGTGCG 483
Db 108 GGACTTGCACCAAGTGTGCTGGAGCTGACTATTGTTGACCTAACAAATTGGTGTGACACTCTCT 167
QY 484 AATGGTGAATTGGTGTCAAGTGTTCGAAACGGTCCTCTTGTGTTAGTAACGTCCTTGAA 543
Db 168 AATGCCGAATTAGCGGCCAGACATTCGCCCATGCTCCTCAGATCAGCAACGCTATGAA 227
QY 544 TTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGCACAGCTAAACCCAGAA 603
Db 228 ATGGATGTTCTTACTGTTAAAGGGAACTTGTGACTTGTTCAAAGACACAAACTCCGAG 287
QY 604 TTGTTCTATGGAGTGTAGGAGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGAATT 663
Db 288 CTGTTTTTGGGTTTATAGGAGTCTCGGGCAGTTTGGGATTATAACAAGAGCAAGGATC 347
QY 664 GTTTTGGACCATGCACCTAAACGGGCCAAATGTTTCGGATGCTCTACAGTGATTTTACA 723
Db 348 GCTCTAGAACCGGCACCAAAAGAGTAAATGGATACAGATGCTTTACGATGACTTCTCC 407
QY 724 ACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGACTAT 783
Db 408 ACATTTCTAGAGACCAAGAACATTGATTTCAAT-----CAATGGACTGGACTAT 458
QY 784 TTAGAAGGTCAAATATTTCTATCAAAACGGGTGCTGTTGACACCT 826
Db 459 TTGGAAGGTTCACTCTTGATGCAAAATAGTTCTCCTATAACT 501

RESULT 13

BU025625 601 bp mRNA linear EST 23-AUG-2002
LOCUS QHG10G19.yg.ab1 QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA
DEFINITION clone QHG10G19, mRNA sequence.

ACCESSION

BU025625
BU025625.1 GI:22461145

VERSION

KEYWORDS

SOURCE

ORGANISM

Helianthus annuus (common sunflower)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

REFERENCE

AUTHORS

1 (bases 1 to 601)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compenomics.ucdavis.edu/
Unpublished (2002)

JOURNAL

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgdb.ucdavis.edu/ for details.
Plate: QHG10 row: G column: 19.

FEATURES

source

Location/Qualifiers
1..601
/organism="Helianthus annuus"
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/cultivar="RHA280"
/db_xref="taxon:4232"
/clone="QH10G19"
/lab_host="E.coli"
/clone_lib="QH_EFGHJ sunflower RHA280"
/note="Vector: pBRCDNASFIAB; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=chemical induction
TAG_LIB=QH_EFGHJ sunflower RHA280
TAG_SEQ=TGTAGCCGGG"

ORIGIN

Query Match 12.4%; Score 186.8; DB 13; Length 601;
Best Local Similarity 63.5%; Pred. No. 3.1e-40;
Matches 306; Conservative 0; Mismatches 167; Indels 9; Gaps 1;

QY 364 TACGCTGACGTGGCGGCCGACGCTTATGGTGGATGTGCTTAAGAAGACGGCGGAGAAA 423
Db 116 TATGCAGATGTTGGAGGTGAGCAGTTATGGATAGATGTTCTTGAAGCTACGTTATGCTAT 175
QY 424 GGGGTGTCGCCGGTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTGTGCG 483
Db 176 GGACTTGCACCGGTTTTCATGGACGGATTACTTGTACCTCACGGTTGGTGAACACTCTCT 235
QY 484 AATGGTGAATTGGTGGTCAAGTGTTCGAAACGGTCCTCTTGTAGTAACGTCCTTGAA 543
Db 236 AATGCTGGGATTAGTGGACAAACATCTTTTCATGGGCTCAAGTTAGCAATGTTCTTGAA 295
QY 544 TTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGCACAGCTAAACCCAGAA 603
Db 296 ATGGATGTCATTACTGGGAAAGGTGATTGTGATAACTTGTCTTAAGGACATGAACCTCTGAT 355
QY 604 TTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGAATT 663
Db 356 CTCCTTTTATGCTGTTCTTGGAGGACTTGGCCAGTTTGGGATCATAAAGTAGGCAAGGATT 415
QY 664 GTTTTGGACCATGCACCTAAACGGGCCAAATGTTTCGGATGCTCTACAGTGATTTTACA 723
Db 416 GTTCTAGACAAGGCACCCCAATAGGGTGAAATGGTTTAAATAAATTTACGACGATTTTGCC 475
QY 724 ACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGACTAT 783
Db 476 AAGTTTCAAAAGGATCAAGAACGTCCTGATATC-----CGTTGATGGGTTTGATAT 526
QY 784 TTAGAAGGTCAAATATTTCTATCAAAACGGGTGCTGTTGACACCTCTTTTCCACCTTCA 843
Db 527 GTAGAAGGCTCTTTTGATCTTGAATAAATAGTCTCTGCAGACAGCTTTTCTCACCTTCTAAT 586
QY 844 GA 845
Db 587 GA 588

RESULT 14

LOCUS

DEFINITION

BQ588342 451 bp mRNA linear EST 06-DEC-2002
E012308-024-008-P04-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-008-P04 5-PRIME, mRNA sequence.

ACCESSION BQ588342
VERSION BQ588342.1 GI:26117925
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1 (bases 1 to 451)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 451 Std Error: 0.00
Plate: 8 row: P column: 04
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES
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/cultiivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:184499"
/db_xref="taxon:161934"
/clone="024-008-P04"
/tissue type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 12.3%; Score 185.2; DB 13; Length 451;
Best Local Similarity 66.6%; Pred. No. 7.4e-40;
Matches 265; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 362 AGTACGCTGACGTGGCGCGGACGTTATGGGTGGATGTGCTTAAGAAGACGGCGGAGA 421
Db 48 AGTATGTAGATGTATGGGGAGGGGAATTATGGGTAGATGTGTTAAAGTGTACGTAGAGT 107

QY 422 AAGGGTGTGCGCGGTTTCTTGACCGGATTATTGTCATATAACCGTCGGAGGAACGTTGT 481
Db 108 ATGGACTCGCACCTAAATCATGCACTGATTATTGTTATCTAACGGTGGGTGCTACGTTGT 167

QY 482 CGAATGGTGAATTGGTGGTCAAGTGTTCGAAACGGTCCCTCTTGTAGTAACGTCCTTG 541
Db 168 CTATGTGGAATTAGTGGACAGCTTTTAATCATGGTCTCTCAATTAGTAACGTTTGT 227

QY 542 AATTGGACGTTATTACTGGGAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCAG 601
Db 228 AGCTTATGTTGTTACAGGAATGAGAGCTTGTGACCTTGTCTTGAGAAGAAAATTCGG 287

QY 602 AATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTGGAATTATACGAGAGCCAGAA 661
Db 288 AGTTGTTTCATGCTGTTTGGGAGGTTTAGGCCAATTGGTATATTACTCGTGTAGGA 347

QY 662 TTGTTTGGACCATGCACCTAAACGGGCCAAATGGTTTGGATGCTCTACAGTGATTTC 721
Db 348 TTGCCCTTGAACCTTCTCTCAACGGGTGAGGTGGATAAGAGTGTGTACTCCAATTTC 407

QY 722 CAACCTTTTACAAAGGACCAAGAACGTTTGTATATCAATG 759
Db 408 CGGCGTTTACAAAGAGATCAAGAGTACTTTAATATCGTTG 445

RESULT 15
CD843876
LOCUS
DEFINITION RFO2.134G18F011010 RFO2 Brassica napus cDNA clone RFO2134G18, mRNA sequence.
ACCESSION CD843876
VERSION CD843876.1 GI:32525816
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 707)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

FEATURES
Location/Qualifiers
1..707
/organism="Brassica napus"
/mol_type="mRNA"
/cultiivar="samourai (restored line)"
/db_xref="taxon:3708"
/clone="RFO2134G18"
/tissue type="anthers"
/clone_lib="RFO2"

ORIGIN
Query Match 12.0%; Score 180.6; DB 14; Length 707;
Best Local Similarity 55.4%; Pred. No. 1.7e-38;
Matches 395; Conservative 0; Mismatches 309; Indels 9; Gaps 2;

QY 712 AGTGATTTCAACACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATAT- 770
Db 1 ACTGATTTCTCTGAATTCACAGAGATCAAGAACGATTGATATCAGAAACGGACGGTTTA 60

QY 771 --TGGAGTCGACTATTTAGAAGGTCAAATATTTCTATCAAAACGGTGTGTTGACACTCT 828
Db 61 CATTTCTTGGAAAGGTTCCGTTATGCTTGACCATGGCCACCTGATAACTGGAGATCTACT 120

QY 829 TTTTCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATC 888
Db 121 TACTATCCACCGTCCGATCACTTGAGGATCGTCTCAATGATCAACCGATACCGTGTATC 180

QY 889 TATGTTCTTGAAGTAGCCAAAGTATTATGATGATCCCAATCTCCCCATCATCAGCAGGTT 948
Db 181 TACTGTCTCGAAGTCGCCAAGTATTACGACGAAACTTCTCAACACTCAGTCAACGAGGAA 240

QY 949 ATTGACACATTAACGAAACATTAAAGTTACTTCCCGGGTTTATATCAATGCACGACGTG 1008
Db 241 ATTGAGAAGTTAAGCGAGAGTTTGAACATATGTAAGAGGGTTTGTACGAGAAAGATGTG 300

QY 1009 GCCTACTTCGATTTCTTGAACCGGTGTACATGTGCGAAGAAAATAAATCTCAGATCTTTGGGA 1068
Db 301 ACGTATATAGATTTCTTGAACCGGGTTCGAACGGGAGAGCTAAACCTGAAATCCAAAGGC 360

Search completed: April 7, 2004, 05:49:25
Job time : 4281 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 02:38:39 ; Search time 144 Seconds
(without alignments)
5803.861 Million cell updates/sec

Title: US-10-014-101-26
Perfect score: 1506
Sequence: 1 atggctaatttcgtttaat.....cagggaagacatcttttga 1506

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	318.6	21.2	1602	3	US-09-124-541-10
2	318.6	21.2	1602	4	US-09-663-326-10
3	185.2	12.3	1605	3	US-09-124-541-3
4	185.2	12.3	1605	4	US-09-663-326-3
5	108.2	7.2	6733	3	US-09-124-541-2
6	108.2	7.2	6733	4	US-09-663-326-2
7	40.4	2.7	832	4	US-09-621-976-2813
8	39	2.6	474	4	US-09-621-976-18033
9	38.6	2.6	7218	1	US-08-232-463-14
10	38	2.5	7218	1	US-08-232-463-14
11	37.6	2.5	4403765	3	US-09-103-840A-2
12	37.6	2.5	4411529	3	US-09-103-840A-1
13	35.6	2.4	1441	4	US-09-004-838-39
14	35	2.3	699	4	US-09-134-001C-812
15	35	2.3	1500	4	US-09-004-838-28
16	35	2.3	11056	4	US-09-004-838-23
17	35	2.3	12793	4	US-09-004-838-124
18	35	2.3	15062	4	US-09-004-838-89
19	34	2.3	399	4	US-09-621-976-8976
20	34	2.3	615	3	US-08-998-416-186
21	34	2.3	636	3	US-08-998-416-1137
22	34	2.3	837	3	US-08-998-416-288
23	33.8	2.2	1173	4	US-09-894-844-60
24	33.8	2.2	4403765	3	US-09-103-840A-2
25	33.6	2.2	832	4	US-09-621-976-2813
26	33.6	2.2	2211	4	US-09-134-001C-818
27	33.6	2.2	2220	4	US-09-543-681A-2265

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29	33.4	2.2	1174	4	US-09-849-242A-3
30	33.2	2.2	474	4	US-09-621-976-18033
31	33	2.2	1166	4	US-09-072-596-323
32	33	2.2	1166	4	US-09-072-967-328
33	33	2.2	1445	4	US-09-510-543-10
34	32.8	2.2	6866	4	US-10-204-708-20
35	32.6	2.2	425	4	US-09-621-976-15651
36	32.6	2.2	7387	4	US-09-238-356-28
37	32.4	2.2	421	3	US-08-642-274D-55
38	32.4	2.2	421	3	US-08-952-014C-55
39	32.4	2.2	985	4	US-09-056-556-182
40	32.4	2.2	985	4	US-09-072-596-177
41	32.4	2.2	985	4	US-09-072-967-182
42	32.4	2.2	1419	4	US-09-266-965-61
43	32.4	2.2	4466	4	US-09-410-551B-20
44	32.4	2.2	4478	4	US-09-410-551B-16
45	32.4	2.2	4547	4	US-09-410-551B-22

ALIGNMENTS

RESULT 1
US-09-124-541-10
; Sequence 10, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: variation
; LOCATION: (6)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (9)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (12)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (21)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (24)
; OTHER INFORMATION: a,g,c or t
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; NAME/KEY: variation
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; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (30)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (33)
; OTHER INFORMATION: a,g,c or t

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FEATURE:
NAME/KEY: variation
LOCATION: (36)
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NAME/KEY: variation
LOCATION: (42)
OTHER INFORMATION: a,g,c or t
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NAME/KEY: variation
LOCATION: (48)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (54)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (57)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (60)
OTHER INFORMATION: a,c,g or t
FEATURE:
NAME/KEY: variation
LOCATION: (63)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (66)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (69)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (72)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (75)
OTHER INFORMATION: a,g,c or t
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NAME/KEY: variation
LOCATION: (78)
OTHER INFORMATION: a,g,c or t
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NAME/KEY: variation
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NAME/KEY: variation
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NAME/KEY: variation
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LOCATION: (96)
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NAME/KEY: variation
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NAME/KEY: variation
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NAME/KEY: variation
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FEATURE:
NAME/KEY: variation
LOCATION: (111)
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NAME/KEY: variation
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OTHER INFORMATION: a,g,c or t
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NAME/KEY: variation
LOCATION: (117)
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NAME/KEY: variation
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FEATURE:
NAME/KEY: variation
LOCATION: (135)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (141)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (144)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (147)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (153)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (159)
OTHER INFORMATION: a,c,g or t
FEATURE:
NAME/KEY: variation
LOCATION: (162)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (165)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (168)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
LOCATION: (171)
OTHER INFORMATION: a,g,c or t
FEATURE:
NAME/KEY: variation
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; LOCATION: (174)
; OTHER INFORMATION: a,g,c or t
; FEATURE:
; NAME/KEY: variation
; LOCATION: (177)
; OTHER INFORMATION: a,g,c or t

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Query Match	21.2%;	Score 318.6;	DB 3;	Length 1602;
Best Local Similarity	36.7%;	Pred. No. 7.5e-96;		
Matches 543; Conservative	230;	Mismatches 636;	Indels 72;	Gaps 8;

[illegible]

Db	1025	CNGCNGCNGCNGTNGAYCARGARYTNGCNWSNGTNYTNGGNACNYTNWSNTAYGTNGARG	1084
Qy	986	GGTTCATATCAATGCACGACGTGGCCTACTTCGATTTCTTGAACCGTGTACATGTGCGAAG	1045
Db	1085	GNITYGCNTTYCARMENGAYGTNGCNTAYGCGNCNTTYTNGAYMGNGTNCAYGGNGARG	1144
Qy	1046	AAAATAAACTCAGATCTTTGGGATTATGGGAACCTTCCTCATCCTTGGCTTAACCTCTACG	1105
Db	1145	ARGTNGCNYTNAAYARYTNGGNYTNTGGMNGTNCNCAYCCNTGGYTNAAATGTTTYG	1204
Qy	1106	TTCCATAAATCTCGGATTCTCGATTTTCATAAACGGTGTGTGCAAGACATTTCTTTAAGC	1165
Db	1205	TNCCMGNWSMGNATHGCGNGAYTTYGAYMGNGGNGTNTTYAARGGNATHYTNC--ARG	1261
Qy	1166	AAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCAAACAAACCGGAATAAATGGGACAATC	1225
Db	1262	GNACNGAYATHGTNGGCCNYTNATHGTNTAYCCNYTNAAYARWSNATGTGGGAYGAYG	1321
Qy	1226	GTATGTCGGCGATGATACCGAGATCGATGAAGATGTTATATATATATTATCGGACTACTAC	1285
Db	1322	GNATGWSNGCNGCNACNCC--NWSNGARGAYGTNTTYTAGCNGTNSNYTNTNTTYW	1378
Qy	1286	AATCCGCTACCCCAAAGGATCTTCCAGAAAGTGGAGAGCGTTAACGAGAAAGATAATTAGGT	1345
Db	1379	SNWSNGTNGCNCNAAYGAYYTNGCNGMNYTNCARGARCARAAYMGNMGNATHYTNMGNT	1438
Qy	1346	TTTGTCAAGGATTCAGGTATTAAGATTAAAGCAATATCTAATGCATTATACGTAAAGAAG	1405
Db	1439	TYTGYGAYYTNGCNGGNATHCARTAYAARACNTAYYTNGCNGMNCNAYACNGAYMGNWSNG	1498
Qy	1406	ATTGGATTGACCATTTTGGAT--CAAAATGGGATGATTTTTTCGAAGACGAAAGATCTAT	1462
Db	1499	AYTGGGTNMGCNAYTTYGGNGCNGCNAARTGGAAVMGNTTYGTNGARATGAARAAYART	1558
Qy	1463	TTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCTTT	1503
Db	1559	AYGAYCCNAAARMGNYTNTNWSNCCNGGNCARGAYATHTTY	1599

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RESULT 2
US-09-663-326-10
; Sequence 10, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: variation
; LOCATION: (6)
; OTHER INFORMATION: a,g,c or t
; NAME/KEY: variation
; LOCATION: (9)
; OTHER INFORMATION: a,g,c or t
; NAME/KEY: variation
; LOCATION: (12)
; OTHER INFORMATION: a,g,c or t
; NAME/KEY: variation
; LOCATION: (21)
; OTHER INFORMATION: a,g,c or t
; NAME/KEY: variation
; LOCATION: (24)
; OTHER INFORMATION: a,g,c or t

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NAME/KEY: variation	LOCATION: (27)	OTHER INFORMATION: a,g,c or t
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NAME/KEY: variation	LOCATION: (33)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (36)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (42)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (48)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (54)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (57)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (60)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (63)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (66)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (69)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (72)	OTHER INFORMATION: a,g,c or t
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NAME/KEY: variation	LOCATION: (78)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (81)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (90)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (93)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (96)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (105)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (108)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (111)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation	LOCATION: (114)	OTHER INFORMATION: a,g,c or t
NAME/KEY: variation		

785	Db	TYWSNGCNGAYCARGARMGNYTNACNGCNCNCNGGNGGNGGNGCNCWSNTTYG	844
788	Qy	AA-----GGTCAATAATTTCTATCAAAACGGTGTGCG	817
845	Db	GNCCNATGWSNTAYGTNGARGGNWSNGTNTTYGTNAAYCARWSNYTNGCNACNGAYYTN	904
818	Qy	TTGACACCTCTTTTTTCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAAC	877
905	Db	CNAAYACGGNTTYTYACNGAYGCGAYGTNGCNCNMGNATHGTNGCNYTNGCNGGNGARM	964
878	Qy	ACGGT-----ATCATCTATGTTCTTGAAAGTAGCCAAAGTATTATGATGATCCCAATCTCC	931
965	Db	GNAAYGCNACNACNGTNTAYWSNATHGARGCNCACNYTNAAYTAYGAYAAAGCNACNGCNG	1024
932	Qy	CCATCA-----TCAGCAAGGTTATTGACACATTAAACGAAAAACATTAAAGTTACTTGCCCG	985
1025	Db	CNGCNGCNGCNGTNGAYCARGARYTNGCNCWSNGTNYTNGGNACNYTNWSNTAYGTNGARG	1084
986	Qy	GGTTCATATCAATGCACGACGTGGCCTACTTCGATTTCTTGAACCGGTACATGTCGAAG	1045
1085	Db	GNTTYGCTTYCARMGNGAYGTNGCNTAYGCGNCNTYYTNGAYMGNGTNCAYGCGNGARG	1144
1046	Qy	AAAAATAAACTCAGATCTTTGGGATTATGGGAACCTTCCTCATCTCTTGGCTTAACCTCTACG	1105
1145	Db	ARGTNGCNYTNAAYARYTNGGNYTNTGGMNGTNCNCNCAICNTGGYTNAAYATGTTYG	1204
1106	Qy	TTCTCTAAATCTCGGATTCGATTTTCATAACGGTGTGTCAAAAGACATTCCTCTTAAGC	1165
1205	Db	TNCCNMGNWSNMGNATHGCGAYTTYGAYMNGGNGTNTTYAARGGNATHYTNC--ARG	1261
1166	Qy	AAAAATCAGCTTCGGGACTCGCTCTCTCTATCCACAAACCCGGAATAAATGGGACAATC	1225
1262	Db	GNACNGAYATHGTNGGNCNYTNATHGTNTAYCCNYTNAAYARWSNATGTGGGAYGAYG	1321
1226	Qy	GTATGTCGGCGATGATACGAGATCGATGAAGATGTTATATATATATATTCGGACTACTAC	1285
1322	Db	GNATGWSNGCNCNACNCC---NWSNGARGAYGNTNTTYAYGCGNGTNSNYTNTTYW	1378
1286	Qy	AATCCGCTACCCCAAAGGATCTTCAGAAAGTGGAGAGCGTTAACGAGAAGATAATTAGGT	1345
1379	Db	SNWSNGTNGCNCNCAAYGAYYTNCGNCMGNYTNCARGARCARAAVMGNMGNATHYTNMGT	1438
1346	Qy	TTTGCAAGGATTCAGGTATTAAGATTAAGCAATATCTAATGCATTATACTAGTAAAGAAG	1405
1439	Db	TYTGYGAYYTNCGNGGNATHCARTAYAAARACNTAYYTNGCNCMGNCAACNGAYMGNWSNG	1498
1406	Qy	ATTGATTGAGCATTTTGGAT--CAAAATGGGATGATTTTTCGAAGAGGAAAGATCTAT	1462
1499	Db	AYTGGGTNMGNCAYYTYGGNGCNCNAARTGGAAVMGNTTYGTNGARATGAARAAYART	1558
1463	Qy	TTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCTTT	1503
1559	Db	AYGAYCNAARMGNYTNTYTNWSNCCNGNCARGAYATHTTY	1599

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RESULT 3
US-09-124-541-3
; Sequence 3, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays

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Db 245 TGGCGCTGCTGAGCGCGGCCAACTCCACCCCGGGTGGCCCTACACCATCGCGTTCGCGG 304
QY 266 GCCAAGGCACTCCTTAAACGGCCAAAGCCTCGGTCTCCGGGGAGTAATCGTCAACATGA 325
Db 305 GCGCGGCACTCCTCATGGGCCAGGCCTTCGCCCCCGCGGCGTCTGCTCAACATGG 364
QY 326 CGTGTATCACTGACGTGGTG-----GTTTCAAAAGACAAGAGTACG 367
Db 365 CGTCCCTGGCGACGCCGCCGCCCGCGCATCAACGTGTCGCGGACGCCGCTACG 424
QY 368 CTGACGTGGCGCGGACGTTATGGTGGATGTGCTTAAAGAGACGGCGGAGAAAGGG 427
Db 425 TGGACGCCGCGGAGCAGGTGTGGATCGACGTGTTGCGCGCGTCTGTCGCGCGCGG 484
QY 428 TGTCCGCGGTTCTTGGACGGATTATTGTCATATAACCGTCGAGGAACGTTGTGCAATG 487
Db 485 TGGCGCGCGCTCCTGGAACGACTACCTTACCTCACCGTCGCGGACGCTGTCCCAAG 544
QY 488 GTGGAATTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTGTAGTAACGTCTTGAATTGG 547
Db 545 CAGGCATCAGCGCCAGGCGTTCGCCACAGCCCCACAGATATCTAACGTGTGGAGATGG 604
QY 548 ACGTTATTCTGGGAAAGGTGAATGTGACATGCTCGCGACAGCTAAACCCAGAATTGT 607
Db 605 ACGTTATCACCGCCATGGGGAGATGGTACGTGCTCCAAGCAGCTGAACGCGGACCTGT 664
QY 608 TCTATGGAGTGTAGGAGGTTTGGGTCAATTTGGAATTATACGAGAGCCAGAATTGTT 667
Db 665 TCGACGCCGCTCTGCGCGGGCTGGGGCAGTTCGAGTGATCACCGGGCCCCGATCGCGG 724
QY 668 TGGACCATGACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTCAACAATT 727
Db 725 TGGAGCCGCGCGCGCGCGCGCGTGGGTGCGGTTCGTGTACACGACTTCGCGGCGT 784
QY 728 TTACAAAGGACCAAGAACGTTTGTATATCAATGGCAACGATATTGGAGTCGACTATTAG 787
Db 785 TCAGCGCCGACCAAGGAGCGGTGACCGCCCGCGCGCGCGCGCGCGCGTTCGTTTCG 844
QY 788 --AAGGTCAAATATTTCTATCAACCGGTGCTGTGACACCTCTTTTTCACCTTCAGA 845
Db 845 GCGCGATGAGCTACGTGGAAGGTCGGTGTCTGTAACCAAGAGCTGGCGACCGACCTGG 904
QY 846 TCAA-----TCTAAGTTCGCTGATCTAGTCAAGCAACACCGGTATCA 886
Db 905 CGAACACGGGTTCTTCAACGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGC 964
QY 887 TCTATGTTCTTGAAGTACCAAGTATTATGATGATCCCAATCTCCCATCATCA----- 940
Db 965 GGAACGCCACCAACCGGTACAGCATCGAGGCGACGCTCAACTACGACCAACGCCACGGCG 1024
QY 941 -----GCAAGGTTATTGACACATTAACGAAACATTAAGTTACTTGCCCG 985
Db 1025 CGGCGCGCGGTGGACAGGAGCTCGCGTCCGTGCTGGCAGCGCTGAGCTACGTGGAGG 1084
QY 986 GGTTCATATCAATGCAAGACGTCGCGCTACTTCGATTCTTGAACCGGTGACATGTCGAAG 1045
Db 1085 GGTTCGCTTCCAGCGGACGTCGCGCTACGCGCGGTCTCTTGACCGGTGACGCGGAGG 1144
QY 1046 AAAATAAACTCAGATCTTTGGGATTATGGGAATTCCTCATCTTGGCTTAACCTCTACG 1105
Db 1145 AGGTGGCGCTCAACAAGCTGGGCTGTGGCGGGTGCAGCACCCGCTGGCTCAACATGTTTCG 1204
QY 1106 TTCCTAATCTCGGATTCTCGATTCTTCATAACGCTGTGTCAAAAGACATTTCTTTAAGC 1165
Db 1205 TGCCGCGCTCGCGCATCGCCGACTTCGACCGCGGCGGTGTTCAAGGSCATCTGTC--AGGG 1262
QY 1166 AAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCAAACAAACCGGAATAAATGGACAATC 1225
Db 1263 CACCGACATCGTCGGCCCGCTCA--TCGTCTACCCCTCAACAAATCCATGTGGGACGACG 1321
QY 1226 GTATGTCGGCGATGATACAGAGATCGATGAAGATGTTATATATATTATCGGACTACTAC 1285

Db 1322 GCATGTCGGCGGCGACGCC---GTCTGAGGACGTGTTCTACCGGTGTGCTCTTCT 1378
QY 1286 AATCCGTACCCCAAGGATCTTCCAGAAGTGGAGAGCGTTAAACGAGAAGATAATTAGGT 1345
Db 1379 CGTCGGTGGCGCCCAACGACCTGGCGAGGCTGCAGGAGCAGACAGGAGATCCTGCGCT 1438
QY 1346 TTTGCAAGGATTGAGTATTAAAGATTAAAGCAATATCTAATGCATTATAGTAAAGAAG 1405
Db 1439 TCTGCGACCTCGCCGGATCCAGTACAAGACCTACCTGGCGCGCACACGACCGCAGTG 1498
QY 1406 ATTGGATTGAGCATTTTGG---ATCAAAATGGGATGATTTTTCGAAGAGAAAGATCTAT 1462
Db 1499 ACTGGTCCGCCACTTCGGCGCCGCAAGTGGAAATCGCTTCGTGGAGATGAAGAACAAGT 1558
QY 1463 TTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCTT 1502
Db 1559 ACGACCCCAAGAGGCTGCTCTCCCCCGCCAGGACATCTT 1598

RESULT 5

US-09-124-541-2
; Sequence 2, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6733
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(6733)
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea
; OTHER INFORMATION: mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1497)..(2111)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2524)..(3216)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3311)..(3607)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (5697)
US-09-124-541-2

Query Match 7.2%; Score 108.2; DB 3; Length 6733;
Best Local Similarity 54.5%; Pred. No. 6.6e-25;
Matches 274; Conservative 0; Mismatches 208; Indels 21; Gaps 2;

QY 89 CCCTTAACCTCACCCCTCTTACCGATCCTTCCATCATCTCCGACGCTCTCATGACTTCG 148
Db 1621 CCTGGACGGCAAGCTCCGACCGACAGCAACGCGACGGCGGGCTCGACGACTTCG 1680
QY 149 GAAACATAACCAACCGTGACCCCGGGGGGTAAATCTGCCCTCTCCACCGCTGATATCT 208
Db 1681 GCAACATCACGTGCGGCTCCCGGGGGGTCTCTGTACCCGCTGCCACGCGGACCTGG 1740
QY 209 CTCGTCTCTCCAATACGCGG---CAAACGGAAGAAAGTACATTCCAAGTAGCGGCTCGT 265
Db 1741 TGGCGCTGTGAGCGCGGCAACTCCACCCCGGGGTGGCCCTACACCATCGGTTCCGCG 1800
QY 266 GCCAAGGCCACTCTTTAAAGGCGCAAGCCTCGGTCTCCGGGGAGTAATCGTCAACATGA 325

Db 1801 GCGCGGCACTCCCTCATGGGCCAGGCTTCGCCCCCGGGCGTCTCGTCAACATGG 1860
QY 326 CGTGATACACTGACGTGGTG-----GTTTCAAAAGACAAGAGTACG 367
Db 1861 CGTCCCTGGCGACCGCCGCGCGCGCATCAACGTGTCCGCGGACGGCGCTACG 1920
QY 368 CTGACGTGGCGCGCGGACGTTATGGGTGGATGTGCTTAAGAAGACGCGGAGAAAGGGG 427
Db 1921 TGGACGCCGCGGCGGAGCAGGTGTGGATCAGCTGTTCGCGCGTCTGGCGCGCGG 1980
QY 428 TGTCCCGCGTTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTGTCGAATG 487
Db 1981 TGGCGCCGCGCTCCTGGAACGACTACCTTACCTACCGTCGGCGGACGCTGTCCAACG 2040
QY 488 GTGGAATTGGTGGTCAAGTGTTCGAAACCGTCTCTTGTAGTAACGTCCTTGAATTGG 547
Db 2041 CAGGCATCAGCGGCCAGCGCTTCGCCACCGCCACAGATATCTAACGTCGCTGGAGATGG 2100
QY 548 ACGTTATTACTGGGAAAGGTGAA 570
Db 2101 ACGTTATCACCGGTACGTGTGCA 2123

RESULT 6
US-09-663-326-2
; Sequence 2, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6733
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(6733)
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea
; OTHER INFORMATION: mays
; NAME/KEY: CDS
; LOCATION: (1497)..(2111)
; NAME/KEY: CDS
; LOCATION: (2524)..(3216)
; NAME/KEY: CDS
; LOCATION: (3311)..(3607)
; NAME/KEY: unsure
; LOCATION: (5697)
US-09-663-326-2

Query Match 7.2%; Score 108.2; DB 4; Length 6733;
Best Local Similarity 54.5%; Pred. No. 6.6e-25;
Matches 274; Conservative 0; Mismatches 208; Indels 21; Gaps 2;
QY 89 CCCTTAACCTCACCCTCTCTACCGATCCTTCCATCATCTCCGAGCCCTCTCATGACTCG 148
Db 1621 CCTTGGACGGCAAGCTCCGGACCGACAGCAACGCGACGGCGGGCCCTCGACGGACTCG 1680
QY 149 GAAACATAACACCGTGACCCCGGGCGGTAACTCGCCCTCTCCACCGCTGATATCT 208
Db 1681 GCAACATCAGTCGGCGCTCCCGGGCGGTCCTGTACCCGTCGTCCACGGCGACCTGG 1740
QY 209 CTCGTCTCTCAATACGCCG---CAAACGGAAAAAGTACATTCCAAGTAGCGGCTCGTG 265
Db 1741 TGGCGCTGCTAGCGCGGCCAACTCCACCCCGGGGTGGCCCTACACCATCGGTTCCGCG 1800

QY 266 GCCAAGGCCACTCCTTAAACGGCCAGCCTCGGTCTCCGGCGGAGTAATCGTCAACATGA 325
Db 1801 GCGCGGCCACTCCCTCATGGGCCAGGCTTCGCCCCCGGGCGTCTCGTCAACATGG 1860
QY 326 CGTGATACACTGACGTGGTG-----GTTTCAAAAGACAAGAGTACG 367
Db 1861 CGTCCCTGGCGACCGCCGCGCGCATCAACGTGTCCGCGGACGGCGCTACG 1920
QY 368 CTGACGTGGCGCGGACGTTATGGGTGGATGTGCTTAAGAAGACGCGGAGAAAGGGG 427
Db 1921 TGGACGCCGCGGCGGAGCAGGTGTGGATCAGCTGTTCGCGCGTCTGGCGCGCGG 1980
QY 428 TGTCCCGCGTTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTGTCGAATG 487
Db 1981 TGGCGCCGCGCTCCTGGAACGACTACCTTACCTACCGTCGGCGGACGCTGTCCAACG 2040
QY 488 GTGGAATTGGTGGTCAAGTGTTCGAAACCGTCTCTTGTAGTAACGTCCTTGAATTGG 547
Db 2041 CAGGCATCAGCGGCCAGCGCTTCGCCACCGCCACAGATATCTAACGTCGCTGGAGATGG 2100
QY 548 ACGTTATTACTGGGAAAGGTGAA 570
Db 2101 ACGTTATCACCGGTACGTGTGCA 2123

RESULT 7
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 2.7%; Score 40.4; DB 4; Length 832;
Best Local Similarity 14.5%; Pred. No. 0.0071;
Matches 53; Conservative 146; Mismatches 167; Indels 0; Gaps 0;
QY 1012 TACTTCGATTCTTGAACCGGTGACATGTGGAAGAAAATAAATACTCAGATCTTTGGGATTA 1071
Db 40 WRRKKKAWKWKYKWTWYWRVAMWGTYYKKAMCRTTKKKKKKKGYMMWYWGWRRSYM 99
QY 1072 TGGGAACCTTCCTCATCTTGGCTTAACCTCTACGTTCTTAATAATCTCGGATTCTCGATT 1131
Db 100 AMWTRTWIGYAYYRSMYWRVRCWKKKAYYRKTTCYSSKGWTTWKRWKAWTTWWKKT 159
QY 1132 CATAACGGTGTGTCAAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTT 1191
Db 160 YYWAATRYWMMWMTKWRASWYICWWWGKARKWSTWRKSRYSASARSAXRCCYSCSNGA 219
QY 1192 CTCTATCCAAACAAACCGGAATAAATGGGACAATCGTATGTCCGGCGATGATACCAGAGATC 1251
Db 220 MSWKYMRMRWRGWATGAGMKAWRASCMRMRKYAGKSKTSYKSMWMCWTRSWKYCYTKA 279
QY 1252 GATGAAGATGTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCA 1311
Db 280 RWTGYCYRKGGMWGRGRWYASKYMWKRWVWVWCMARMYRISTGTASMWRRWRYTMM 339
QY 1312 GAAGTGGAGAGCGCTTAACGAGAAGATAATTAGGTTTTTGCAGGATTTCAGGTATTAGATT 1371

COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 2.5%; Score 38; DB 1; Length 7218;
Best Local Similarity 2.2%; Pred. No. 0.23;
Matches 8; Conservative 200; Mismatches 150; Indels 0; Gaps 0;
QY 351 AAAAGACAAGTACGCTGACGTGGCGGCGGACGTTATGGTGGATGGTAAAGAA 410
Db 1413 RRR 1354
QY 411 GACGGCGAGAAAGGGGTGTCGCGGTTTCTTGGACGGATTATTGTCATATAACGTCGG 470
Db 1353 RRR 1294
QY 471 AGGAACGTGTCGAATGGTGAATGGTGGTCAAGTGTTCGAAACGGTCTCTTTAG 530
Db 1293 RRR 1234
QY 531 TAACGTCCTTGAATTGGACGTTATTACTGGGAAAGTGAATGTTGACATGCTCGGACA 590
Db 1233 RRR 1174
QY 591 GCTAAACCCAGAAATGTTCTATAGGAGTGTAGGAGTTTGGTCAATTGGAATTAAAC 650
Db 1173 RRR 1114
QY 651 GAGAGCCAGAAATGTTTGGACCATGCACCTAAACGGGCCAAATGTTTCGGATGCTC 708
Db 1113 RRR 1056

RESULT 11
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.5%; Score 37.6; DB 3; Length 4403765;
Best Local Similarity 45.1%; Pred. No. 33;
Matches 139; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
QY 366 CGTGACGTGGCGGCGGACGTTATGGTGGATGCTTAAAGAACGCGGAGAAAGG 425
Db 4154796 CGCCACGTGGCGGCGGATGTCACATACGAGGACCTAATCGCCGACACTGACG 4154855
QY 426 GGTGTCGCGGTTCTTGGACGGATTATTTGCATATAACCGTCGGAGGAACGTTGTCGAA 485
Db 4154856 TCTGTACCATTTGGTGGTTCGCGAGCTGAGGACGATCAGATTTGGCGGAGCGTCACCGG 4154915
QY 486 TGTGGAATTTGGTCAAGTGTTCGAAACGGTCTCTTTGTTAGTAACGTCCTTGAATT 545
Db 4154916 CTTGGGTATCGAGTCGGCGTCTCCGCAACGGCTGCCCCACGAGTCGGTGTGGAGAT 4154975
QY 546 GGACGTTATTACTGGGAAAGCTGAAATGTTGACATGCTCGGACAGCTAAACCCAGAAATT 605
Db 4154976 GGATATCTCACCAGCGGCGGAGAGAACTTCTCACCGCTCGCCCGGACAGCACTCCGACTT 4155035
QY 606 GTTCTATGGAGTGTAGGAGGTTGGGTCAATTTGGATTTAATTAACGAGAGCCAGAAATTGT 665
Db 4155036 GTACCGTGATTCCTTAACCTGATGGGACACTGGGGCTATTCAACCCGGCTTCGATCCA 4155095
QY 666 TTTGGACC 673
Db 4155096 GCTGGAGC 4155103

RESULT 12
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 2.5%; Score 37.6; DB 3; Length 4411529;
Best Local Similarity 45.1%; Pred. No. 33;
Matches 139; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
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Db 4162545 CGCCGACGTGGCCGGCATGTGCACATACGAGGACCTAATCGCCGGACACTGCCTACGG 4162604
QY 426 GGATCGCCGGTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAAACGTTGTCGAA 485
Db 4162605 TCTGTCACCATGGTGGTTCCGACGCTGAGGACGATCACATTGGCGGAGCGGTACCCGG 4162664
QY 486 TGGTGAATGGTGGTCAAGTGTTCGAAACGGTCCTCTTTGTAGTAACGTCCTTGAATT 545
Db 4162665 CTTGGGTATCGAGTCGGCGTCTTCGCAACGGCTTCCGCCACGAGTCGGTGTGGAGAT 4162724
QY 546 GGACGTTATTAATCTGGGAAAGGTGAATGTTGACATGCTCGGACAGCTAAACCCAGAATT 605
Db 4162725 GGATATCTCACCGGCGCAGGAGAACTTCTCACCGTCTCGCCCGACAGCACTCCGACTT 4162784
QY 606 GTTCTATGAGTGTAGGAGGTTTGGGTCAATTGGAATTATAACGAGAGCCAGAAATTGT 665
Db 4162785 GTACCGTGCATTCCTTAACCTCGTATGGGACACTGGGCTATTCAACCCGGCTTCGAATCCA 4162844
QY 666 TTTGGACC 673
Db 4162845 GCTGGAGC 4162852

RESULT 13
US-09-004-838-39/c
; Sequence 39, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Conferring Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1441 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..1441
; OTHER INFORMATION: /note= "RLG2M"
US-09-004-838-39

Query Match 2.4%; Score 35.6; DB 4; Length 1441;
Best Local Similarity 63.9%; Pred. No. 0.43;
Matches 53; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 883 ATCATCTATGTTCTTGAAGTAGCCAAAGTATTATGATGATCCCAATCTCCCATCATCAGC 942
Db 237 ATCAACTAATTCGCAACATCGTCAAGTANTATGAGGAACCTTAGCTTACCTCCATCTGA 178
QY 943 AAGGTTATTGACACATTAAACGAA 965
Db 177 ATTCTTTTGAACCATTCACGAA 155
RESULT 14
US-09-134-001C-812/c
; Sequence 812, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 812
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-812
Query Match 2.3%; Score 35; DB 4; Length 699;
Best Local Similarity 49.2%; Pred. No. 0.4;
Matches 92; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 1038 TGTGGAAGAAATAAATCACTCAGATCTTTGGGATTATGGGAACCTTCCTCATCTTGGCTTAA 1097
Db 194 TGTCTTATCAAAATCAAGTGTAAATTATCTACAATAGGAACCTTGATTTTCTCAGCATAA 135
QY 1098 CCTCTACGTTCTCTAAATCTCGGATTCTCGATTTTTCATAACGGTGTGTCAAGACATTCT 1157
Db 134 ACTTAAGTTCTTCGATTTCAGTATCAATTGATGATGTAATTTGCTAAATATTTTGA 75
QY 1158 TCTTAAGCAAAATCAAGTTCGGGACTCGCTCTTCTCTATCCAAACACCGGAATAAATG 1217
Db 74 TTGTAATCCATATCATTTAAACTTCCTTTATCATTAACAATTACAAAACAAATAAATC 15
QY 1218 GGACAAAT 1224
Db 14 AGCCCAT 8
RESULT 15
US-09-004-838-28/c
; Sequence 28, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Conferring Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 04:38:13 ; Search time 607 Seconds
(without alignments)
9298.375 Million cell updates/sec

Title: US-10-014-101-26
Perfect score: 1506
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2470632 seqs, 1873875610 residues 4941264

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1506	100.0	1506	12	US-10-311-453-26 Sequence 26, Appl
2	1506	100.0	1506	14	US-10-014-101-26 Sequence 26, Appl
3	1504.4	99.9	1506	14	US-10-326-184-8 Sequence 8, Appli
4	778.2	51.7	1575	9	US-09-938-842A-2089 Sequence 2089, Ap
5	778.2	51.7	1575	11	US-09-938-842A-2089 Sequence 2089, Ap
6	778.2	51.7	1575	12	US-10-311-453-28 Sequence 28, Appl
7	778.2	51.7	1575	14	US-10-014-101-28 Sequence 28, Appl
8	778.2	51.7	1575	14	US-10-326-184-10 Sequence 10, Appl
9	778.2	51.7	1655	14	US-10-326-184-20 Sequence 20, Appl
10	577	38.3	2991	12	US-10-311-453-3 Sequence 3, Appli
11	577	38.3	2991	14	US-10-014-101-3 Sequence 3, Appli
12	470	31.2	1572	12	US-10-311-453-27 Sequence 27, Appl
13	470	31.2	1572	14	US-10-014-101-27 Sequence 27, Appl
14	470	31.2	1572	14	US-10-326-184-9 Sequence 9, Appli
15	306.2	20.3	1611	12	US-10-311-453-29 Sequence 29, Appl

16	306.2	20.3	1611	14	US-10-014-101-29	Sequence 29, Appl
17	306.2	20.3	1620	12	US-10-311-453-34	Sequence 34, Appl
18	306.2	20.3	1620	14	US-10-014-101-34	Sequence 34, Appl
19	306.2	20.3	1623	14	US-10-326-184-12	Sequence 12, Appl
20	248.8	16.5	1728	12	US-10-311-453-25	Sequence 25, Appl
21	248.8	16.5	1728	14	US-10-014-101-25	Sequence 25, Appl
22	237.4	15.8	1857	14	US-10-326-184-22	Sequence 22, Appl
23	233.6	15.5	1318	12	US-10-424-599-9802	Sequence 9802, Ap
24	225.8	15.0	2782	12	US-10-311-453-7	Sequence 7, Appli
25	225.8	15.0	2782	14	US-10-014-101-7	Sequence 7, Appli
26	172	11.4	3302	12	US-10-311-453-5	Sequence 5, Appli
27	172	11.4	3302	14	US-10-014-101-5	Sequence 5, Appli
28	171.6	11.4	1575	14	US-10-326-184-11	Sequence 11, Appl
29	171.6	11.4	1873	14	US-10-326-184-21	Sequence 21, Appl
30	171.4	11.4	566	14	US-10-326-184-14	Sequence 14, Appl
31	171	11.4	1515	12	US-10-311-453-30	Sequence 30, Appl
32	171	11.4	1515	14	US-10-014-101-30	Sequence 30, Appl
33	169.8	11.3	635	14	US-10-326-184-16	Sequence 16, Appl
34	168.2	11.2	582	14	US-10-326-184-18	Sequence 18, Appl
35	164.4	10.9	2235	12	US-10-424-599-78119	Sequence 78119, A
36	151.8	10.1	1141	12	US-10-425-114-10886	Sequence 10886, A
37	151.8	10.1	1142	12	US-10-424-599-1725	Sequence 1725, Ap
38	148.4	9.9	1384	12	US-10-425-114-8799	Sequence 8799, Ap
39	144.4	9.6	1023	12	US-10-425-114-10804	Sequence 10804, A
40	144.4	9.6	1045	12	US-10-424-599-19583	Sequence 19583, A
41	143.2	9.5	552	14	US-10-326-184-15	Sequence 15, Appl
42	137.2	9.1	1257	12	US-10-425-114-3248	Sequence 3248, Ap
43	123.8	8.2	2805	12	US-10-311-453-9	Sequence 9, Appli
44	123.8	8.2	2805	14	US-10-014-101-9	Sequence 9, Appli
45	123.8	8.2	2814	12	US-10-311-453-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-10-311-453-26

; Sequence 26, Application US/10311453

; Publication No. US20040031073A1

; GENERAL INFORMATION:

; APPLICANT: Schmling, Thomas

; APPLICANT: Werner, Tom s

; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and

; TITLE OF INVENTION: physiology

; FILE REFERENCE: 1226-4

; CURRENT APPLICATION NUMBER: US/10/311,453

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: EP 00870132.8

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: US 60/258,415

; PRIOR FILING DATE: 2000-12-27

; PRIOR APPLICATION NUMBER: EP 01870053.4

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 26

; LENGTH: 1506

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-10-311-453-26

Query Match 100.0%; Score 1506; DB 12; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCTAATCTTCGTTTAAATGATCACTTTTAAATCAGGTTTTTAAATGATCACCAAAATCATCA	60
Db	1	ATGCTAATCTTCGTTTAAATGATCACTTTTAAATCAGGTTTTTAAATGATCACCAAAATCATCA	60
QY	61	AACGGTATTAAATTTGATTACCTTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC	120
Db	61	AACGGTATTAAATTTGATTACCTTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCC	120

QY 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACATAACCAACCGTGACCCCGCGGCGTA 180
Db 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACATAACCAACCGTGACCCCGCGGCGTA 180
QY 181 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCTCCCAATACGCCGCAACCGGA 240
Db 181 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCTCCCAATACGCCGCAACCGGA 240
QY 241 AGTACATTCGAAGTAGCGGCTCGTGCCCAAGGCCACTCCTTAAACGCCCAAGCCTCGGTC 300
Db 241 AGTACATTCGAAGTAGCGGCTCGTGCCCAAGGCCACTCCTTAAACGCCCAAGCCTCGGTC 300
QY 301 TCCGGCGAGTAATCGTCAACATGACGCTGATFACACTGACGTGGTGGTTTCAAAAGACAAG 360
Db 301 TCCGGCGAGTAATCGTCAACATGACGCTGATFACACTGACGTGGTGGTTTCAAAAGACAAG 360
QY 361 AAGTACGCTGACGTGGCGGCCGGGACGTTATGGGTGGATGTGCTTAAGAAGACGCGGAG 420
Db 361 AAGTACGCTGACGTGGCGGCCGGGACGTTATGGGTGGATGTGCTTAAGAAGACGCGGAG 420
QY 421 AAAGGGGTGTCGCCGGTTCTTGGACGGATTATTTGCATATAACCGTCGGAGGAACGTTG 480
Db 421 AAAGGGGTGTCGCCGGTTCTTGGACGGATTATTTGCATATAACCGTCGGAGGAACGTTG 480
QY 481 TCGAATGGTGAATGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACGTCCTT 540
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QY 541 GAATTGGACGTTATTACTGGGAAGGTGAATGTTGACATGCTCGCGACAGCTAAACCCA 600
Db 541 GAATTGGACGTTATTACTGGGAAGGTGAATGTTGACATGCTCGCGACAGCTAAACCCA 600
QY 601 GAATTGTTCTATGGAGTGTAGGAGGTTTGGGTCAATTTGGAATATATAACGAGAGCCAGA 660
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QY 661 ATTGTTTGGACCATGCACCTAAACCGGCCAAATGGTTTCGGATGCTCTACAGTATTTC 720
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QY 721 ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATATGGAGTCGAC 780
Db 721 ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATATGGAGTCGAC 780
QY 781 TATTTAGAAGGTCAAATATTCTATCAAAACGGTGTGCTTGACACCTCTTTTCCACCT 840
Db 781 TATTTAGAAGGTCAAATATTCTATCAAAACGGTGTGCTTGACACCTCTTTTCCACCT 840
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Db 841 TCAGATCAATCTAAAGTCGTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA 900
QY 901 GTAGCCAAGTATTATGATGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTA 960
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QY 1201 ACAAAACCGGAATAAATGGGACAATCGTATGTGCGCGATGATACAGAGATCGATGAAGAT 1260

Db 1201 ACAAAACCGGAATAAATGGGACAATCGTATGTGCGCGATGATACAGAGATCGATGAAGAT 1260
QY 1261 GTTATATATATATATCGGACTACTACAAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAG 1320
Db 1261 GTTATATATATATATCGGACTACTACAAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAG 1320
QY 1321 AGCGTTAACGAGAAGATAAATAGGTTTGGCAAGGATTGAGCATTTTGGATCAAAATGGGATAT 1380
Db 1321 AGCGTTAACGAGAAGATAAATAGGTTTGGCAAGGATTGAGCATTTTGGATCAAAATGGGATAT 1380
QY 1381 CTAATGCATTATATACTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATAT 1440
Db 1381 CTAATGCATTATATACTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATGGGATAT 1440
QY 1441 TTTTCGAAGAGGAAAGATCTATTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATC 1500
Db 1441 TTTTCGAAGAGGAAAGATCTATTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATC 1500
QY 1501 TTTTGA 1506
Db 1501 TTTTGA 1506

RESULT 2

US-10-014-101-26
; Sequence 26, Application US/10014101
; Publication No. US20030074598A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 26
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-26

Query Match 100.0%; Score 1506; DB 14; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTAATCTTCGTTTAAATGATCACTTTAATCACGSGTTTAAATGATCACCAATCATCA 60
Db 1 ATGGCTAATCTTCGTTTAAATGATCACTTTAATCACGSGTTTAAATGATCACCAATCATCA 60
QY 61 AACGGTATTAAATTTGATTTTACCTTAAATCCCTTAACTTACCTCACCCCTCTCTACCGATCCTTCC 120
Db 61 AACGGTATTAAATTTGATTTTACCTTAAATCCCTTAACTTACCTCACCCCTCTCTACCGATCCTTCC 120
QY 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATACACCGTGACCCCGCGGCGGTA 180
Db 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATACACCGTGACCCCGCGGCGGTA 180
QY 181 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCTCTCCAAATACCGCGCAACCGGAAAA 240
Db 181 ATCTGCCCTCCTCCACCGCTGATATCTCTCGTCTCTCTCCAAATACCGCGCAACCGGAAAA 240
QY 241 AGTACATTCGAAGTAGCGGCTCGTGGCCAAAGGCCACTCTCTTAAACGGCAAGCCTCGGTC 300

Db 241 AGTACATCCAAAGTAGCGGCTCGTGGCCAAAGCCACTCCTTAAACGGCCAAAGCCTCGGTC 300
QY TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAAGACAAG 360
Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAAGACAAG 360
QY 361 AAGTACCGTGACGTGGCGGCCGGGACGTTATGGTGGATGCTTAAGAAGACGGCGGAG 420
Db 361 AAGTACCGTGACGTGGCGGCCGGGACGTTATGGTGGATGCTTAAGAAGACGGCGGAG 420
QY 421 AAAGGGGTGTCGCCCGGTTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTG 480
Db 421 AAAGGGGTGTCGCCCGGTTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTG 480
QY 481 TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCCCTTGTAGTAAACGTCCTT 540
Db 481 TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCCCTTGTAGTAAACGTCCTT 540
QY 541 GAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCA 600
Db 541 GAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCTAAACCCA 600
QY 601 GAATTGTTCTATGGAGTGTAGGAGGTTGGGTCAATTTGGAATATAACGAGAGCCAGA 660
Db 601 GAATTGTTCTATGGAGTGTAGGAGGTTGGGTCAATTTGGAATATAACGAGAGCCAGA 660
QY 661 ATTGTTTTGGACCATGACCTAAACCGGCGCAATGGTTTCGGATGCTCTACAGTATTC 720
Db 661 ATTGTTTTGGACCATGACCTAAACCGGCGCAATGGTTTCGGATGCTCTACAGTATTC 720
QY 721 ACAACTTTTACAAAGGACCAAGAACGTTTGTATCAATGGCAACGATATTGGAGTCGAC 780
Db 721 ACAACTTTTACAAAGGACCAAGAACGTTTGTATCAATGGCAACGATATTGGAGTCGAC 780
QY 781 TATTTAGAAGGTCAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTTCCACCT 840
Db 781 TATTTAGAAGGTCAAATATTTCTATCAAAACGGTGTGTTGACACCTCTTTTCCACCT 840
QY 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA 900
Db 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA 900
QY 901 GTAGCCAAAGTATTATGATGATCCCAATCTCCCAATCATCAGCAAGGTTATGACACATTA 960
Db 901 GTAGCCAAAGTATTATGATGATCCCAATCTCCCAATCATCAGCAAGGTTATGACACATTA 960
QY 961 ACGAAACATTAAGTTACTTGCCTGGGTTTCATATCAATGACGACGTGGCTACTTCGAT 1020
Db 961 ACGAAACATTAAGTTACTTGCCTGGGTTTCATATCAATGACGACGTGGCTACTTCGAT 1020
QY 1021 TTCTTGAAACCGGTGACATGTCGAAGAAATAAACTCAGATCTTTGGGATTATGGGAACCT 1080
Db 1021 TTCTTGAAACCGGTGACATGTCGAAGAAATAAACTCAGATCTTTGGGATTATGGGAACCT 1080
QY 1081 CCTCATCCTTGGCTTAACCTCTACGTTCTTAAATCTCGGATTCTCGATTTTTCATAACGGT 1140
Db 1081 CCTCATCCTTGGCTTAACCTCTACGTTCTTAAATCTCGGATTCTCGATTTTTCATAACGGT 1140
QY 1141 GTTGTCAAAGACATTTCTTTAAGCAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCA 1200
Db 1141 GTTGTCAAAGACATTTCTTTAAGCAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCA 1200
QY 1201 ACAAAACCGGAATAAATGGGACAAATCGTATGTGCGGCGATGATACCAAGATCGATGAAGAT 1260
Db 1201 ACAAAACCGGAATAAATGGGACAAATCGTATGTGCGGCGATGATACCAAGATCGATGAAGAT 1260
QY 1261 GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAG 1320
Db 1261 GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAG 1320
QY 1321 AGCGTTAACGAGAAGATAATTAGGTTTTCGAAGGATTCAGGTATTAAGATTAAAGCAATAT 1380

Db 1321 AGCGTTAACGAGAAGATAATTAGTTTTCGAAGGATTCAGGTATTAAAGATTAAAGCAATAT 1380
QY 1381 CTAATGCATTATACTAGTAAAGAAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT 1440
Db 1381 CTAATGCATTATACTAGTAAAGAAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT 1440
QY 1441 TTTTCGAAGAGGAAAGATCTATTGATCCCAAGAACTGTTATCTCCAGGGCAAGACATC 1500
Db 1441 TTTTCGAAGAGGAAAGATCTATTGATCCCAAGAACTGTTATCTCCAGGGCAAGACATC 1500
QY 1501 TTTTGA 1506
Db 1501 TTTTGA 1506
RESULT 3
US-10-326-184-8
; Sequence 8, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C3
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-8

Query Match 99.9%; Score 1504.4; DB 14; Length 1506;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTAATCTTCGTTTAATGATCACTTTAATACGGTTTAATGATCACCATAATCATCA 60
Db 1 ATGCTAATCTTCGTTTAATGATCACTTTAATACGGTTTAATGATCACCATAATCATCA 60
QY 61 AACGTTATTAATAATTGATTACCTAAATCCCTTAACTACCTACCCCTCTCTACCGATCCTTCC 120
Db 61 AACGTTATTAATAATTGATTACCTAAATCCCTTAACTACCCCTCTCTACCGATCCTTCC 120
QY 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATTAACACCGTGAACCCCGCGGCGTA 180
Db 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATTAACACCGTGAACCCCGCGGCGTA 180
QY 181 ATCTGCCCTCCTCCACCGCTGATATCTCTGTCCTCTCCAAATACGCCGCAACGGAATA 240
Db 181 ATCTGCCCTCCTCCACCGCTGATATCTCTGTCCTCTCCAAATACGCCGCAACGGAATA 240
QY 241 AGTACATTCCAAGTAGCGGCTCGTGGCCAAAGGCCACTCCTTAAACGGCCAAGCCTCGGTC 300
Db 241 AGTACATTCCAAGTAGCGGCTCGTGGCCAAAGGCCACTCCTTAAACGGCCAAGCCTCGGTC 300
QY 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAAGACAAG 360
Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGGTGGTTTCAAAAGACAAG 360
QY 361 AAGTACGCTGACGTGGCGGCCGGGACGTTATGGTGGATGCTTAAGAAGACGGCGGAG 420
Db 361 AAGTACGCTGACGTGGCGGCCGGGACGTTATGGTGGATGCTTAAGAAGACGGCGGAG 420
QY 421 AAAGGGGTGTCGCCCGGTTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTG 480
Db 421 AAAGGGGTGTCGCCCGGTTTCTTGGACGGATTATTGTCATATAACCGTCGGAGGAACGTTG 480
QY 481 TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAAACGTCCTT 540

Db 481 TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCCCTCTTGTAGTAACGTCCTT 540
QY 541 GAATGGACGTTATTAAGGAAAGGTAAGTGTGACATGCTCGGACAGCTAAACCCA 600
Db 541 GAATGGACGTTATTAAGGAAAGGTAAGTGTGACATGCTCGGACAGCTAAACCCA 600
QY 601 GAATGGTCTATGAGTGTTAGGAGGTTTGGGTCAATTTGGAATTAACGAGAGCCAGA 660
Db 601 GAATGGTCTATGAGTGTTAGGAGGTTTGGGTCAATTTGGAATTAACGAGAGCCAGA 660
QY 661 ATTGTTTTGGACCATGACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTATTTC 720
Db 661 ATTGTTTTGGACCATGACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTATTTC 720
QY 721 ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGAC 780
Db 721 ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGAC 780
QY 781 TATTTAGAAGGTCAAAATATTTCTATCAACCGGTGCTGTGACACCTCTTTTCCACCT 840
Db 781 TATTTAGAAGGTCAAAATATTTCTATCAACCGGTGCTGTGACACCTCTTTTCCACCT 840
QY 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA 900
Db 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAA 900
QY 901 GTAGCCAAAGTATTATGATGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTA 960
Db 901 GTAGCCAAAGTATTATGATGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTA 960
QY 961 ACGAAACATTAAGTTACTTGCCCGGGTTTCATATCAATGCACGACGTGGCCTACTTCGAT 1020
Db 961 ACGAAACATTAAGTTACTTGCCCGGGTTTCATATCAATGCACGACGTGGCCTACTTCGAT 1020
QY 1021 TTTCTGAACCGTGTACATGTGCAAGAAATAAACTCAGATCTTTGGGATTTATGGGAACCTT 1080
Db 1021 TTTCTGAACCGTGTACATGTGCAAGAAATAAACTCAGATCTTTGGGATTTATGGGAACCTT 1080
QY 1081 CTTTCATCCTTGGCTTAAACCTTACGTTTCTTAAATCTCGATTTCTCGATTTTTCATAACGGT 1140
Db 1081 CTTTCATCCTTGGCTTAAACCTTACGTTTCTTAAATCTCGATTTCTCGATTTTTCATAACGGT 1140
QY 1141 GTTGTCAAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCA 1200
Db 1141 GTTGTCAAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCA 1200
QY 1201 ACAACCGGAATAAATGGGACAAATCGTATGTGCGCGATGATACCAGAGATCGATGAAGAT 1260
Db 1201 ACAACCGGAATAAATGGGACAAATCGTATGTGCGCGATGATACCAGAGATCGATGAAGAT 1260
QY 1261 GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGAG 1320
Db 1261 GTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGAG 1320
QY 1321 AGCGTTAACGAGAAAGATAATTAGGTTTTCGAAGGATTCAGGATTAAGATTAAGCAATAT 1380
Db 1321 AGCGTTAACGAGAAAGATAATTAGGTTTTCGAAGGATTCAGGATTAAGATTAAGCAATAT 1380
QY 1381 CTAATGCATTATAC TAGTAAAGAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT 1440
Db 1381 CTAATGCATTATAC TAGTAAAGAGATTGGATTGAGCATTTTGGATCAAAATGGGATGAT 1440
QY 1441 TTTTCGAAGAGGAAAGATCTATTTGATCCCAAGAACTGTTATCTCCAGGGCAAGACATC 1500
Db 1441 TTTTCGAAGAGGAAAGATCTATTTGATCCCAAGAACTGTTATCTCCAGGGCAAGACATC 1500
QY 1501 TTTTGA 1506
Db 1501 TTTTGA 1506

RESULT 4

US-09-938-842A-2089
; Sequence 2089, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2089
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2089

Query Match 51.7%; Score 778.2; DB 9; Length 1575;
Best Local Similarity 72.2%; Pred. No. 4.1e-223;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;

QY 42 AATGATCACCAAATCATCAACGGTATTAAATTTACCTAAATCCCTTAACCTCAC 101
Db 63 AACCTTAATCAATCAGATGAGGCGATTGATGTTTCTTACCATATCACTCACTTAC 122
QY 102 CCTCTCTACCGATCCTTCCATCATCTCCGACGCTCTCATGACTTCGGAACATAACCAC 161
Db 123 GGTCTTAACCGATCCCTTCTCCATCTCTGCCGCTTCTCAGGACTTCGGTAACATAACCGA 182
QY 162 CGTAGCCCCCGGCGGTAAATCTGCCCCCTCCTCCACGCTGATATCTCTCGTCTCTCTCC- 220
Db 183 CGAAATCCCGCGCCGCTCTCTGCCCTTCTCCACACGAGGTGGCTCGTCTCTCTCCG 242
QY 221 -----AATACGCCGCAACGGAAAAAGTACATTCCA 251
Db 243 TTTTCGCTAACGGAGGATCTCTTACAATAAAGGCTCAACAGCCCCGGCTCTACTTTCAA 302
QY 252 AGTAGCGCTCGTGGCCAAAGGCACTCCTTAAACGGCCAAAGCCTCGGTCTCCGGCGGAGT 311
Db 303 AGTGGCTGCTCGAGGCCAAGGCCACTCCCTCCGTGGCCAAAGCCTCTGCACCCCGGAGGTGT 362
QY 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA 353
Db 363 CGTCGTGAACATGACGTGTCTCGCCATGGCGGCTAAACAGCGCGGTTGTTATCTCGGC 422
QY 354 AGACAAGAGTACGTGACGTGGCGCCGGGACGTTTATGGGTGGATGTGCTTAAAGAGAC 413
Db 423 AGACGGGACTTACGTGACGTGGCTGCTCGCGGACGATGTGGGTGGATGTTCTGAAGGCGGC 482
QY 414 GGCGGAGAAAGGGGTGTCCCGGTTTCTTGGACGGATTAATTTGCATATAACCGTCGGAGG 473
Db 483 GGTGGATAGAGCGTCTCGCCGTTTACATGGACGGATTAATTTGTATCTCAGCGTCGGCGG 542
QY 474 AACGTTGTGCAATGGTGGAAATTTGGTGTCAAGTGTTCGAAACGGTCTCTTGTAGTAA 533
Db 543 GACGTTGTGCAACGCTGGAATCGGTGTGTGCTCAGACGTTTAGACAGGCCCTCAGATTAGTAA 602
QY 534 CGTCTTGAATTTGACGTTTATCTGGAAGGTTGAAATGTTGACATGCTCGGACAGCT 593
Db 603 CGTTCAATGAGCTTACGTTTATTACCGGAAAGGTTGAAATGATGACTTGCTCTCCAAAGTT 662
QY 594 AAACCCAGAAATTTCTATGGAGTGTAGGAGGTTTGGGTCAATTTGGAATTAACGAG 653
Db 663 AAACCTGAATTTCTATGGAGTTTAGGAGGTTTGGGTCAATTTGGGTATTATTAACGAG 722

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; FILE REFERENCE: SCSIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2089
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2089

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Query Match	51.7%;	Score 778.2;	DB 11;	Length 1575;
Best Local Similarity	72.2%;	Pred. No. 4.1e-223;		
Matches 1093; Conservative	0;	Mismatches 363;	Indels 57;	Gaps 4;

Query Match		51.7%;	Score 778.2;	DB 11;	Length 1575;
Best Local Similarity		72.2%;	Pred. No. 4.1e-223;		
Matches 1093;		Conservative 0;	Mismatches 363;	Indels 57;	Gaps 4;
QY	42	AATGATCACCAAAATCATCAAACGGTATTAAAAATTGATTTACCTAAATCCCTTAACCTCAC	101		
DB	63	AACCTTAATCAAAATCAGATGAGGGCATTGATGTTTCTTACCCATATCACTCAACCTTAC	122		
QY	102	CCTCTCTACCGATCCTTCCATCATCTCCGACGCTCTCATGACCTTCGGAACATAAACCCAC	161		
DB	123	GGTCCTAACCGATCCCTTCTCCATCTCTGCCGCTTCTCAGACCTTCGGTAACATAAACCCGA	182		
QY	162	CGTGACCCCGCGGGCGTAATCTGCCCTCTCCACCGCTGATATCTCTCGTCTCCTCC-	220		
DB	183	CGAAATCCCGCGCGCTCTCTGCCCTTCTCCACACGGAGGTGGCTCGTCTCCTCCG	242		
QY	221	-----AATACGCCGCAACCGAAAGTACATTCCA	251		
DB	243	TTTCGCTAACGGAGGATTCTCTTACAATAAAGGCTCAACAGCCCGCTCTACTTTCAA	302		
QY	252	AGTAGCGGCTCGTGGCCAAAGGCCACTCCTTAAACGGCCAAGCCTCGGTCTCCGGCGGAGT	311		
DB	303	AGTGGCTGCTCGAGGCCAAAGGCCACTCCCTCCGTGGCCAAGCCTCTGCACCCCGGAGGTGT	362		
QY	312	AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA	353		
DB	363	CGTCGTGAACATGACGTGTCTCGCCATGGCGGCTAAACAGCGCGGTTGTTATCTCGC	422		
QY	354	AGACAAGAAAGTACGCTGACGTGGCGCGCGGACGTTATGGTGGATGTCTTAAGAAGAC	413		
DB	423	AGACGGGACTTACGCTGACGTGGCTGCCGGGACGATGTGGTGGATGTTCTGAAGCGCGC	482		
QY	414	GGCGGAGAAAGGGTGTCCCGGTTTCTTGGACGGATTATTTGCATATAACCGTCGGAGG	473		
DB	483	GGTGGATAGAGGCTCTCGCCGGTTACATGGACGGATTATTTGTATCTCAGCGTCGCGG	542		
QY	474	AACGTTGTCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAA	533		
DB	543	GACGTTGTCGAACGCTGGAAATCGGTGGTCAGACGTTTAGACACGGCCCTCAGATTAGTAA	602		
QY	534	CGTCTTGAATTGACGCTTATTACTGGGAAAGGTGAATAATTTGACATGCTCGCGACAGCT	593		
DB	603	CGTTCAATGACCTTGACGTTATTACCGGAAAGGTGAATAATGATGACTTGTCTCCAAAAGTT	662		
QY	594	AAACCCAGAATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAATTATAACGAG	653		
DB	663	AAACCCGAATTGTTCTATGGAGTTTTAGGAGGTTTGGGTCAATTCGGTATTATAACGAG	722		
QY	654	AGCCAGAATTGTTTTGGACCATGCACCTAAACGGGCCAAATAGTTTCGGATGCTCTACAG	713		
DB	723	GGCCAGGATTGCGTTGGATCATGCACCCCAAGGGTGAATAATGTTCTCGCATACTCTACAG	782		
QY	714	TGATTTCAACACTTTTACAAAGGACCAAGAACGTTTGTATATCAATGGCAACGATATTGG	773		
DB	783	TGACTTCTCGGCTTTTAAAGAGACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGG	842		
QY	774	AGTCGACTATTTAGAAAGGTCAAATATTTCTATCAACCGGTGTCGTTGACACCTCTTTT	833		


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843 AGTTGACCTTTTGGAGGTCACCTTATGATGTCAAAGGCTTCGTAGACACCTCTTTCTT 902
834 CCCACCTTCAGATCAATCTAAAGTCGTGATCTAGTCAAGCAACACCGTATCATCTATGT 893
903 CCCACTCTCCGATCAAAAGAGTCGCATCTCTTGTGATGATGACACCGGATCATCTATGT 962
894 TCTTGAAGTAGCCAAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGA 953
963 TCTCGAAGTAGCCAAAGTATTATGACAGAACACACCTTCCCAATATTGACCAAGGTGATTGA 1022
954 CACATTAAACGAAACATTAAGTTACTTCCCGGGTTCATATCAATGACAGCGTGGCCTA 1013
1023 CACGTTAAGTAGAATCTAGGTTTCGCTCCAGGGTTTATGTTGCTACAAGATGTTCCGTA 1082
1014 CTTTCGATTTCTTGAACCGGTGTACATGTCGAAGAAATAAATCAAGATCTTTGGGATATG 1073
1083 TTTTCGATTTCTTGAACCGGTGTCCGAACGAAAGATGATAAATCAAGATCTTTAGGACTATG 1142
1074 GGAACCTTCTCTCATCTTGGCTTAACCTCTACGTTCCCTAAATCTCGGATTTCTCGATTTTCA 1133
1143 GGAAGTTCTCTCATCTTGGCTTAACATCTTGTCCCGGGTCTCGAATCCAAGATTTTCA 1202
1134 TAACGGTGTGTCGAAAGACATTTCTTCTTAAGCAAAATCACTTCCGGACTCGCTCTTCT 1193
1203 TGATGGTGTATTAATGGCTTCTTCTTAACCAACCACTCACTTCTGTTGTTACTCTCTT 1262
1194 CTATCCAAACAAACCGGAATTAATGGGACAAATCGTATGTCGGCGATGATACCAAGATCGA 1253
1263 CTATCCCAACAAACCGGAACAAATGGGACAAACCGCATGTCAACGATGACACC-----GGA 1316
1254 TGAAGATGTTATATATATATATATCGGACTACTACAATCCGC---TACCCCAAGGATCTTCC 1310
1317 CGAAGATGTTTTTATGATCGGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1376
1311 AGAAGTGGAGAGCGTTAAACGAGAAAGATTAATAGGTTTTCGAAGGATTCAGGATTAAGAT 1370
1377 AGAAGTGAATCTCAACGACAGGTTATTCAGTTTGTGAAACCTCGGGAATTAAGAT 1436
1371 TAAGCAATATCTAATGATTAATGATTAATGATTAAGGATGATGATGATGATGATGATGATGAT 1430
1437 TAAGGAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1496
1431 ATGGGATGATTTTTCGAAGAGGAAAGATCTATTGATCCCAAGAAACTGTTATCTCCAGG 1490
1497 ATGGGATGATTTTTCGAAGAGGAAATATTGTTGATCCCAAGAAACTGTTATCTCCAGG 1556
1491 GCAAGACATCTTT 1503
1557 ACAAGACATATTT 1569

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RESULT 6

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US-10-311-453-28
; Sequence 28, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28

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; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-28

Query Match      51.7%; Score 778.2; DB 12; Length 1575;
Best Local Similarity 72.2%; Pred. No. 4.1e-223;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;

QY 42 AATGATCACCAATCATCAACGGTATTAAATTTGATTTACCTAAATCCCTTAACCTCAC 101
Db 63 AACCTTAATCAATCAGATGAGGCGATGATGTTTCTTACCATATCACTCAACCTTAC 122
QY 102 CCTCTCTACCGATCCTTCCATCATCTCCGAGCCTCTCATGATTCGGAAACATAACAC 161
Db 123 GGTCTTAACCGATCCCTTCTCCATCTCTGCGCTTCTCACGACTTCGGTAACATAACGA 182
QY 162 CGTGACCCCGCGCGGTAATCTGCCCTCTCCACCGCTGATATCTCTGTCCTCTCC- 220
Db 183 CGAAATCCCGCGCGCTCTCTGCCCTTCTCCACCAACGAGGTGGCTCTCTCTCCG 242
QY 221 -----AATACCGCGCAACCGGAAAAAGTACATCCA 251
Db 243 TTTCGCTAACCGAGGATTTCTTTACAATAAAGGCTCAACACGCGCGCTCTACTTTCAA 302
QY 252 AGTAGCGGCTCGTGCCCAAGGCCACTCTTAAACGGCCAGCCTCGGTCTCCGGCGGAGT 311
Db 303 AGTGGCTGCTCGAGGCCAAGGCCACTCTCCCTCCGTGGCCAAAGCTCTGCACCCGGAGGT 362
QY 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA 353
Db 363 CGTCGTGAACATGACGTGTCTCGCCATGGCGGCTAAACACGCGCGGTGTTTATCTCGGC 422
QY 354 AGACAAAGAGTACGCTGACGTGGCGGCGCGGACGTTATGCGTGGATGTCTTAAAGAGAC 413
Db 423 AGACGGGACTTACGCTGACGTGGCTGCCGCGGACGATGTGGTGGATGTCTTGAAGCGGC 482
QY 414 GCGGAGAAAGGGGTGTGCCCGTTTCTTGGACGGATTTTGCATATAACCGTCGGAGG 473
Db 483 GGTGGATAGAGGCGTCTCGCCGTTACATGACGCGGATTTTGTATCTCAGCGTCGCGG 542
QY 474 AACGTTGTGAAATGGTGAATTTGGTGTCAAGTGTTCGAAACGGTCTCTTGTGTAGTAA 533
Db 543 GACGTTGTGAAACGCTGGAATCGGTGGTTCAGACGCTTTAGACACGCGCCCTCAGATTAGTAA 602
QY 534 CGTCTTGAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGCGACAGCT 593
Db 603 CGTTCATGAGCTGACGTTATTACCGGAAAGGTGAAATGATGACTTGTCTCTCCAAAGTT 662
QY 594 AAACCCAGAAATTGTTCTATGGAGTTTAGGAGGTTTGGGTCAATTGGAATTATTAACGAG 653
Db 663 AAACCCCTGAATTGTTCTATGGAGTTTAGGAGGTTTGGGTCAATTGGAATTATTAACGAG 722
QY 654 AGCCAGAAATTGTTTGGACCATGCACTTAAACGGGCGCAATGGTTTCGGATGCTCTACAG 713
Db 723 GGCAGGATTTGCGTGGATCATGCAACCCACAGGGTGAAATGGTCTCGCATACTCTACAG 782
QY 714 TGATTTCAACACTTTTACAAAGGACCAAGAACGTTTGTATATCAATGGCAACGATATTGG 773
Db 783 TGACTTCTCGGCTTTTAAAGAGACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGG 842
QY 774 AGTCGACTATTTAGAAAGGTCAAAATATTCTATCAAAACGGTGTGCTTGACACCTCTTTT 833
Db 843 AGTTGACTTTTGGAAAGGTCAACTTATGATGTCAAAATGGCTTCGTAGACACCTCTTTCT 902
QY 834 CCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGT 893
Db 903 CCCACTCTCCGATCAAAACAGAGTCCGATCTCTTGTGATGACCAACCGGATCATCTATGT 962
QY 894 TCTTGAAGTAGCCAAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGA 953
Db 963 TCTCGAAGTAGCCAAAGTATTATGACAGAACCAACCTTCCCATTTGACCAAGGTGATTGA 1022

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1143 GGAAGTTCTCATCCATGGCTTAACATCTTTGTCCCGGGTCTCGAATCCAAGATTTTCA 1202
1134 TAACGGTGTGTCAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTTCT 1193
1203 TGATGGTGTATTAATGGCTTCTTTAAACCAAACTCAACTTCTGGTGTACTCTCTT 1262
1194 CTATCCAAACAAACCGGAATAAATGGGACAATCGPATGTGCGGATGATACCAAGATCGA 1253
1263 CTATCCCAACAAACCGAAACAAATGGAACAACCGCATGTCAACGATGACACC-----GGA 1316
1254 TGAAGATGTTATATATATATCGGACTACTACAATCCGC--TACCCCAAAGGATCTTCC 1310
1317 CGAAGATGTTTTTATGTGATCGGATTACTGCAATCAGCTGGTGATCTCAAAAATTGGCA 1376
1311 AGAAGTGGAGCGGTTAACGAGAAGATAATTAGGTTTTGCAAGGATTCAGGTATTAAGAT 1370
1377 AGAACTTGAAATCTCAACGACAAGGTTATTCAGTTTTGTGAAAACCTCGGGAATTAAGAT 1436
1371 TAAGCAATATCTAATGCATTTACTAGTAAAGAAAGATTGGATTGAGCATTTTGGATCAAA 1430
1437 TAAGGAATATTTGATGCATATACAGAAAGAAAGATTGGTTAAACATTTTGGACCAA 1496
1431 ATGGGATGATTTTTTCGAGAGGAAAGATCTATTTGATCCCAAGAACTGTATCTCCAGG 1490
1497 ATGGGATGATTTTTTAAGAAAGAAATATATGTTTGATCCCAAGAACTATGTCTCCAGG 1556
1491 GCAAGACATCTTT 1503
1557 ACAAGACATATTT 1569

RESULT 8
US-10-326-184-10
; Sequence 10, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-10

Query Match 51.7%; Score 778.2; DB 14; Length 1575;
Best Local Similarity 72.2%; Pred. No. 4.1e-223;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;

QY 42 AATGATCACCAAAATCATCAAAACGGTATTAAAAATTGATTTACCTAAATCCCTTAACCTCAC 101
Db 63 AACCTTAATCAAAATCAGATGAGGGCATTGATGTTTTCTTACCCATATCACTCAACCTTAC 122
QY 102 CCTCTCTACCGATCCTTCCATCATCTCCGAGCCTCTCATGACTTCGGAAACATAACCCAC 161
Db 123 GGTCTTAACCGATCCCTTCTCCATCTCTGCGCTTCTCACGACTTCGGTAACATAACCGA 182
QY 162 CGTGACCCCGCGGGCGTAAATCTGCCCTCCTCCACCGTGTATCTCTCGTCTCCTCC- 220
Db 183 CGAAATCCCGGCGCGTCTCTGCTGCTCTCCACCGAGTGGCTCGTCTCCTCCG 242
QY 221 -----AATACGCCGCAACCGGAAAGCTCAACCGCCCGGCTACTTTCAA 251
Db 243 TTTGCTAACGGAGGATTCTCTTACAATAAAGGCTCAACCGCCCGGCTACTTTCAA 302

QY 252 AGTAGCGGCTCGTGCCAAAGGCCACTCCTTAAACGGCCAAAGCCTCGTCTCCGGCGGAGT 311
Db 303 AGTGGCTGCTCGAGGCCAAAGGCCACTCCCTCGTGCGCCAAAGCCTCTGCACCCGGAGGTGT 362
QY 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA 353
Db 363 CGTCGTGAACATGACGTGTCTCGCCATGCGCGGTAAACCAAGCGCGGTGTATCTCGGC 422
QY 354 AGACAAGAAGTACGCTGACGTGGCGGCCGGGACGTTATGGGTGATGTGCTTAAGAAGAC 413
Db 423 AGACGGGACTTACGCTGACGTGGCTGCCGGGACGATGTGGGTGATGTTCGAAGGCGGC 482
QY 414 GCGCGAGAAAGGGGTGTCGCCGGTTTTCTTGGACGGATTATTTGCATATAAACGTCGGAGG 473
Db 483 GGTGGATAGAGCGCTCTCGCCGGTTACATGGACGGATTATTTGTATCTCAGCGTCGGCGG 542
QY 474 AACGTTGTGCAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCCCTCTTGTAGTAA 533
Db 543 GACGTTGTGCAACGCTGGAATCGGTGGTCAGACGTTTAGACACGCGCCCTCAGATTAGTAA 602
QY 534 CGTCCTTGAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACAGCT 593
Db 603 CGTTCATGAGCTTGACGTTATTACCGGAAAGGTGAAATGATGACTTGTCTCCAAAGTT 662
QY 594 AAACCCAGAAATTGTTCTATGGAGTGTTAGGAGGTTTGGGTCAATTTGGAAATTATAACGAG 653
Db 663 AAACCCCTGAATTGTTCTATGGAGTTTTTAGGAGGTTTGGGTCAATTCGGTATTATAACGAG 722
QY 654 AGCCAGAAATTGTTTGGACCATGCACCTAAACCGGCCAAATGGTTTTCGGATGCTCTACAG 713
Db 723 GGCCAGGATTGCGTTGGATCATGCACCCCAAGGGTGAATGGTCTCGCATACTCTACAG 782
QY 714 TGATTTCAAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGG 773
Db 783 TGACTTCTCGGCTTTTAAAGAGACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGG 842
QY 774 AGTCGACTATTTAGAAAGTCAAAATATTTCTATCAACGGTGTGCTTGACACCTCTTTTTT 833
Db 843 AGTTGACTTTTGGAAAGGTCAACTTATGATGTCAAAATGGCTTCGTAGACACCTCTTCTT 902
QY 834 CCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACCGGTATCATCTATGT 893
Db 903 CCCACTCTCCGATCAAAACAAAGAGTCGCATCTCTTTGGAATGACCCCGGATCATCTATGT 962
QY 894 TCTTGAAGTAGCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGA 953
Db 963 TCTCGAAGTAGCCAAGTATTATGACAGAACCAACCCCTTCCCATTATTGACCAAGGTGATTGA 1022
QY 954 CACATTAAACGAAAAACATTAAAGTACTTGTCCCGGGTTCAATATCAATGCACGACGTGGCCTA 1013
Db 1023 CACGTTAAAGTAGAACTCTAGGTTTCGCTCCAGGGTTTATGTTCTGTAAGATGTTCCGTA 1082
QY 1014 CTTGATTTCTTGAACCGGTACATGTGGAAGAAAAATAAATCAATCTTTGGGATATATG 1073
Db 1083 TTTTCGATTTCTTGAACCGGTGTCGAAACGAAAGATAAACTCAGATCTTTTAGGACTATG 1142
QY 1074 GGAACCTCCTCATCCTTGGCTTAAACCTCTACGTTCTCTAAATCTCGGATTTCTCGATTTTCA 1133
Db 1143 GGAAGTTCCTCATCCATGGCTTAAACATCTTTGTCCCGGGTCTCGAATCCAAGATTTTCA 1202
QY 1134 TAACGGTGTGTCAAAGACATTTCTTCTTAAGCAAAAAATCAGGCTTCGGGACTCGCTCTTCT 1193
Db 1203 TGATGGTGTATTAAATGGCTTCTTCTTAAACCAACCTCAACTTCTGGTGTACTCTCTT 1262
QY 1194 CTATCCAAACAAACCGGAATAAATGGGACAATCGTATGTCCGGGATGATACCAAGATCGA 1253
Db 1263 CTATCCCAACAAACCGAAACAAATGGAACCAACCGCATGTCAACGATGACACC-----GGA 1316
QY 1254 TGAAGATGTTATATATATTATCGGACTACTACAATCCGC---TACCCCAAAGGATCTTCC 1310
Db 1317 CGAAGATGTTTTTATGTGATCGGATTACTGCAATCAGCTGGTGGATCTCAAAATTGGCA 1376
QY 1311 AGAAGTGGAGACCGTTAACGAGAGATAATTAGGTTTTTGCAGGATTCAGGTATTAAAGAT 1370

Db 1377 AGAACTTGAAAACTCAACGACACAGGTATTTCAGTTTGTGAAAACTCGGGAATTAAGAT 1436
QY 1371 TAAGCAATATCTAATGCATTATATACTAGTAAAGAAAGATTGGATTGAGCATTTTGGATCAAA 1430
Db 1437 TAAGGAATATTGATGCACATATACAGAAAAGAGATTGGGTAAACATTTTGGACCAA 1496
QY 1431 ATGGGATGATTTTTCGAAGAGGAAAGATCTATTGTGATCCCAAGAAACTGTTATCTCCAGG 1490
Db 1497 ATGGGATGATTTTAAAGAAAGAAAATTAATGTTGATCCCAAGAACTATTGTCTCCAGG 1556
QY 1491 GCAAGACATCTTT 1503
Db 1557 ACAAGACATATT 1569

RESULT 9
US-10-326-184-20
; Sequence 20, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF Q
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-20

Query Match 51.7%; Score 778.2; DB 14; Length 1655;
Best Local Similarity 72.2%; Pred. No. 4.2e-223;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;

QY 42 AATGATCACCAATCATCAACGGTATTAAAAATTGATTTACCTAAATCCCTTAACCTCAC 101
Db 63 AACCTTAATCAAAATCAGATGAGGCAATTGATGTTTCTTACCATPACACTCAACCTTAC 122
QY 102 CCTCTCTACCGATCCTTCCATCATCTCCGAGCCTCTCATGACTCGGAAACATAACAC 161
Db 123 GGTCCTAACCGATCCCTTCTCCATCTCTCGCGCTTCTCACGACTTCGGTAACATAACCGA 182
QY 162 CGTGACCCCGGGCGTAACTCTGCCCTCTCCACCGCTGATATCTCTGCTCCCTCC - 220
Db 183 CGAAATCCCGGCGCGTCTCTGCCCCTCTCCACCAACGAGGTGGCTCGTCTCCTCCG 242
QY 221 -----AATACGCCGCAACCGGAAAAAGTACATTCCA 251
Db 243 TTTCGCTAACGGAGGATTCTCTTACAATAAAGGCTCAACGAGCCCGCGTCTACTTTCAA 302
QY 252 AGTAGCGGCTCGTGCCCAAGGCCACTCCTTAAACGGCCCAAGCCTCGGTCTCCGGCGGAGT 311
Db 303 AGTGGCTGCTCGAGGCCAAGGCCACTCCCTCCGTGGCCCAAGCCTTGACACCCGGAGGTG 362
QY 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAA 353
Db 363 CGTCGTGAACATGACGTGTCTCGCCATGGCGGCTAAACGAGCGGCGGTGTTATCTCGGC 422
QY 354 AGACAAGAAGTACGTGACGTGGCGGCGGCGGACGTTATGGTGGATGTGCTTAAAGAGAC 413
Db 423 AGACGGGACTTACGCTGACGTGGCTGCCGGGACGATGTGGGTGGATGTTCTGAAGCGCGC 482
QY 414 GCGGAGAAAGGGTGTGCGCGGTTTCTTGACGGATTATTTGCAATAAACCCTCGGAGG 473
Db 483 GGTGGATAGAGCGCTCTCGCCGGTTACATGACGGATTATTTGTATCTCAGCGTCGCGCG 542

QY 474 AACGTTGTGCAATGGTGAATTTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTGTAGTAA 533
Db 543 GACGTTGTGCAACGCTGGAATCGGTGGTCAAGCGTTTAGACACGGCCCTCAGATTAGTAA 602
QY 534 CGTCTTGAATTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGCGACAGCT 593
Db 603 CGTTCATGAGCTTGACGTTATTACCGGAAAAGGTGAAATGATGACTTGCTCTCCAAAGTT 662
QY 594 AAACCCAGAAATTGTTCTATGGAGTGTAGGAGGTTTGGGTCAATTTGGAATTATAACGAG 653
Db 663 AAACCCCTGAATTTCTATGGAGTTTATAGGAGGTTTGGGTCAATTCGGTATTATAACGAG 722
QY 654 AGCCAGAAATTGTTTGGACCATGCACCTAAACGGGCCAAATGGTTCGGATGCTCTACAG 713
Db 723 GGCCAGGATTGCGTTGGATCATGACCCACAAGGTGAAATGGTCTGCATACTCTACAG 782
QY 714 TGATTTCACAACTTTTACAAAGGACCAAGAACGTTTGTATATCAATGGCAACGATATTGG 773
Db 783 TGACTTCTCGGCTTTTAAAGAGACCAAGAGCGGTTTAATATCAATGACCAATGATCTCGG 842
QY 774 AGTCGACTATTAGAAGGTCAAAATATTCTATCAAAACGGTGTCTGTTGACACCTCTTTT 833
Db 843 AGTTGACTTTTGAAGGTCAACTTATGATGTCAAAATGGCTTCGTAGACACCTCTTTCTT 902
QY 834 CCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGT 893
Db 903 CCCACTCTCCGATCAAAACAAGAGTCGCATCTCTTGTGAATGACACCGGATCATCTATGT 962
QY 894 TCTTGAAGTAGCCAAAGTATTATGATGATGCCAAATCTCCCCATCATCAAGGTTATTGA 953
Db 963 TCTCGAAGTAGCCAAAGTATTATGACAGAACCAACCTTCCCATTATTGACCAGGTGATTGA 1022
QY 954 CACATTAACGAAAAACATTAAGTTACTTGGCCGGGTTTATATCAATGACGACGCTGGCCTA 1013
Db 1023 CACGTTAAGTAGAACTCTAGGTTTCGCTCCAGGGTTTATGTTGTCGTAACAAGATGTTCCGTA 1082
QY 1014 CTTCGATTTCTTGAACCGGTGTACATGTCGAAGAAAAATAAACTCAGATCTTTGGGATTATG 1073
Db 1083 TTTCGATTTCTTGAACCGGTGTCCGAAACGAAGAAGATAAACTCAGATCTTTAGGACTATG 1142
QY 1074 GGAACCTTCCTCATCCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATCTCGATTTTCA 1133
Db 1143 GGAAGTTCTCATCCTCATGCTTAAACATCTTGTCCGGGTCTCGAATCCAAGATTTTCA 1202
QY 1134 TAACGGTGTTCGTAAGACATTTCTTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTTCT 1193
Db 1203 TGATGGTGTATTAAATGGCCCTTCTTCTAAACCAACCTCAACTTCTGTTGTTACTCTCT 1262
QY 1194 CTATCCAAACAAACCGGAATAAATGGGACAAATCGTATGTGCGCGATGATACAGAGATCGA 1253
Db 1263 CTATCCCAACAAACCGGAACAAATGGAACACCGCATGTCAACGATGACACC-----GGA 1316
QY 1254 TGAAGATGTTATATATATTATCGGACTACTACAATCCGC--TACCCCAAGGATCTTCC 1310
Db 1317 CGAAGATGTTTTTATGTGATCGGATTACTGCAATCAGCTGGTGGATCTCAAAATTGGCA 1376
QY 1311 AGAAGTGGAGAGCGTTAACGAGAAGATAATTAGGTTTTGCAAGGATTCAGGTATTAAAGAT 1370
Db 1377 AGAACTTGAAAATCTCAACGACAGAGGTTATTTCAGTTTTGTGAAAACTCGGGAATTAAGAT 1436
QY 1371 TAAGCAATATCTAATGCATTATATACTAGTAAAGAAAGATTGGATTGAGCATTTTGGATCAA 1430
Db 1437 TAAGGAATATTTGATGCACCTATACAAGAAAAGAAAGATTGGGTTAAACATTTTGGACCAA 1496
QY 1431 ATGGGATGATTTTTCGAAGAGGAAAGATCTATTGATCCCAAGAAACTGTTATCTCCAGG 1490
Db 1497 ATGGGATGATTTTAAAGAAAAGAAAATTAATGTTTGTATCCCAAGAACTATTGTCTCCAGG 1556
QY 1491 GCAAGACATCTTT 1503
Db 1557 ACAAGACATATT 1569

RESULT 10
US-10-311-453-3
; Sequence 3, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-3

Query Match 38.3%; Score 577; DB 12; Length 2991;
Best Local Similarity 75.9%; Pred. No. 2.6e-162;
Matches 852; Conservative 0; Mismatches 40; Indels 231; Gaps 2;

QY	615	AGTGTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGAAATGTTTGGACCA	674
Db	1869	ACTGTAATATGGTTTCTTTATATATGTGTGTATAAATAATGGGATTGTTTCTCTAAA	1928
QY	675	TGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTCACAACCTTTTACAAA	734
Db	1929	TGAAATTGTGTAGGCCAAATGGTTTCGGATGCTCTACAGTGATTTCACAACCTTTTACAAA	1988
QY	735	GGACCAAGAACGTTTGATATCAATGGCAACGATATTCGAGTCGACTATTAGAAAGGTCA	794
Db	1989	GGACCAAGAACGTTTGATATCAATGGCAACGATATTCGAGTCGACTATTAGAAAGGTCA	2048
QY	795	AATATTCTATCAACCGGTGCTTGACACCTCTTTTCCACCTTCAGATCAATCTAA	854
Db	2049	AATATTCTATCAACCGGTGCTTGACACCTCTTTTCCACCTTCAGATCAATCTAA	2108
QY	855	AGTCGCTGATCTAGTCAAGCAACCGGTATCATCTATGTTCTTGAAGTAGCCAGTATTA	914
Db	2109	AGTCGCTGATCTAGTCAAGCAACCGGTATCATCTATGTTCTTGAAGTAGCCAGTATTA	2168
QY	915	TGATGATCCCAATCTCCCATCATCAGCA	943
Db	2169	TGATGATCCCAATCTCCCATCATCAGCAAGGTACTACACATTTACATTTTCATCATCGT	2228
QY	944	-----	943
Db	2229	TTTTATCATACCATAAGATATTTAAATGATTTCATCATTCGACCACATTAAGATATTCATC	2288
QY	944	-----AGG	946
Db	2289	ATCATCATCGTTACATTTTTTTTGCATCTTATGCTTCTCATAATCTACTATTGTGTAGG	2348
QY	947	TTATTGACACATTAACGAAAAACATTAAAGTTACTTGCCCGGTTTCATATCAATGCACGACG	1006
Db	2349	TTATTGACACATTAACGAAAAACATTAAAGTTACTTGCCCGGTTTCATATCAATGCACGACG	2408
QY	1007	TGGCCTACTTCGATTTCTTGAACCGGTACATGTGCAAGAAAAATAAACTCAGATCTTTGG	1066
Db	2409	TGGCCTACTTCGATTTCTTGAACCGGTACATGTGCAAGAAAAATAAACTCAGATCTTTGG	2468
QY	1067	GATTATGGGAACCTTCCTCATCCTTGCGCTTAACCTCTACGTTCCCTAAATCTCGGATTCCTCG	1126
Db	2469	GATTATGGGAACCTTCCTCATCCTTGCGCTTAACCTCTACGTTCCCTAAATCTCGGATTCCTCG	2528

QY	1127	ATTTTCATAACGGTGTGTCAAAGACATTTCTTTAAAGCAAAAATCAGCTTCGGGACTCG	1186
Db	2529	ATTTTCATAACGGTGTGTCAAAGACATTTCTTTAAAGCAAAAATCAGCTTCGGGACTCG	2588
QY	1187	CTCTTCTCTATCCAAACACCGGAATAA	1214
Db	2589	CTCTTCTCTATCCAAACACCGGAATAAAGTACATACTTCTTTCATTCAATTTATCTTC	2648
QY	1215	-----ATGGGACAA	1223
Db	2649	AAGAACCAGTAATAAATTTCTATGAACCTGATTATGCTGTTATTGTTAGATGGGACAA	2708
QY	1224	TCGTATGTCGGCGATGATACAGAGATCGATGGAAGATGTTATATATATTATTCGGACTACT	1283
Db	2709	TCGTATGTCGGCGATGATACAGAGATCGATGGAAGATGTTATATATATTATTCGGACTACT	2768
QY	1284	ACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAGAGCGTTAACGAGAAAGATAATTAG	1343
Db	2769	ACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAGAGCGTTAACGAGAAAGATAATTAG	2828
QY	1344	GTTTGCAGGATTTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATATACTAGTAAAGA	1403
Db	2829	GTTTGCAGGATTTCAGGTATTAAAGATTAAAGCAATATCTAATGCATTATATACTAGTAAAGA	2888
QY	1404	AGATTGGATTGAGCATTTTGGATCAAAAATGGGATCATTTTTCGAAGAGGAAAGATCTATT	1463
Db	2889	AGATTGGATTGAGCATTTTGGATCAAAAATGGGATCATTTTTCGAAGAGGAAAGATCTATT	2948
QY	1464	TGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCTTTTGA	1506
Db	2949	TGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCTTTTGA	2991

RESULT 11
US-10-014-101-3
; Sequence 3, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-014-101-3

Query Match 38.3%; Score 577; DB 14; Length 2991;
Best Local Similarity 75.9%; Pred. No. 2.6e-162;
Matches 852; Conservative 0; Mismatches 40; Indels 231; Gaps 2;

QY	615	AGTGTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGAAATGTTTGGACCA	674
Db	1869	ACTGTAATATGGTTTCTTTATATATGTGTGTATAAATAAATGGGATTGTTTCTCTAAA	1928
QY	675	TGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGAATTTCAAACTTTTACAAA	734
Db	1929	TGAAATTGTGTAGGCCAAATGGTTTCGGATGCTCTACAGTGAATTTCAAACTTTTACAAA	1988

Publication No. US20040031073A1
GENERAL INFORMATION:
APPLICANT: Schmling, Thomas
APPLICANT: Werner, Tom S
TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
TITLE OF INVENTION: physiology
FILE REFERENCE: 1226-4
CURRENT APPLICATION NUMBER: US/10/311,453
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: EP 00870132.8
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/258,415
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: EP 01870053.4
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 1572
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-311-453-27

Query Match 31.2%; Score 470; DB 12; Length 1572;
Best Local Similarity 58.7%; Pred. No. 2.9e-130;
Matches 881; Conservative 0; Mismatches 600; Indels 21; Gaps 3;

QY 17 TAATGATCAGTCTTTAATCAGCGTTTAAATGATGATCACCATAATCATCAAAACGGTATTAAATG 76
Db 56 TCATCATTAATCTCTCAACTCCGATCAACAACACATCACCAACACCATGGAATATCC 115
QY 77 ATTTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTCCATCATCTCCGAGCCT 136
Db 116 TTTCACACAACGAATTCCGCGGAAAACTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 175
QY 137 CTCATGACTTCGGAAACATAAACACCGTGACCCCGCGCGGCGTAATCTGCCCCCTCTCCA 196
Db 176 CCACAGATTTCCGGCCACGTCACCAAAATCTTCCCTTCCGCGCTCTTAATCCCTCTCTCCG 235
QY 197 CCGCTGATATCTCTGCTCTCTCTCAATACCGCGCAACCGGAAAAAGTACATTCACAGTAG 256
Db 236 TTGAAGACATCACAGATCTCATATAAACTCTCTTTGACTCTCAACTGTCTCTTTCTCTTAG 295
QY 257 CCGCTCGTGCCCAAGGCCACTCTTAAACGGCCAGCCTCGGTCTCCGGCGGAGTAATCG 316
Db 296 CCGCTCGTGTTCACGGACACAGCCACCGTGGCCAGCCTCGGTAAAGACGGAGTGTGG 355
QY 317 TCAACATGACGTGTATCACTGACGTGG-----TGGTTTCAAAAGACAAAGT 364
Db 356 TCAACATGCGGTCCATGGTAAACCGGGATCGAGGTATCAAGGTGTCTAGGACCTGTATT 415
QY 365 ACCTGACGTGGCGCGCGGACGTATGGGTGGATGTGCTTAAGAAAGACGGCGGAGAAAG 424
Db 416 ATGTTGACGTGGACGCTCGGTGGCTATGGATTGAGGTGTGAATAAACTTTGGAGTTAG 475
QY 425 GGGTGTCCCGGTTTCTTGGACGGAATATTGTCATATAACCGTCCGAGGAACGTTGTCCA 484
Db 476 GGTAAACGCGGTTTCTTGGACGGAATATTGTTATTTAACAGTCCGTTGGGACGTTATCAA 535
QY 485 ATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACGTCTCTTGAAT 544
Db 536 ACGGCGGAATAGTGGACAAACGTTTCGGTACGGTCCACAGATCACTAATGTTCTAGAGA 595
QY 545 TGGACGTTATTACTGGGAAAGGTGAATGTTGACATCTCTCGGACAGCTAAACCCAGAAAT 604
Db 596 TGGATGTTATTACTGGAAGAGAGAGATTGCAACTTGTTCACAGGACATGAACCTCGGATC 655
QY 605 TGTTCTATGAGTGTAGGAGGTTTGGGTCAATTTGGAAATTATAACGAGAGCCAGAAATG 664
Db 656 TTTTCTTCCGCGTGTAGGAGGTTTGGGTCAATTCGGCATTTATAACAAGAGCCAGAAATTA 715
QY 665 TTTTGGACCATGCACCTAAACGGGCGCAAAATGGTTTCGGATGCTCTACAGTATTTCACAA 724

QY 735 GGACCAAGAACGTTTGATATCAATGGCAAAACGATATTGGAGTCGACTATTTAGAAGTCA 794
Db 1989 GGACCAAGAACGTTTGATATCAATGGCAAAACGATATTGGAGTCGACTATTTAGAAGTCA 2048
QY 795 AATATTTCTATCAAAACGGTGTGCTTGACACCTCTTTTCCACCTTCAGATCAATCTAA 854
Db 2049 AATATTTCTATCAAAACGGTGTGCTTGACACCTCTTTTCCACCTTCAGATCAATCTAA 2108
QY 855 AGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCCAAAGTATTA 914
Db 2109 AGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCCAAAGTATTA 2168
QY 915 TGATGATCCCAATCTCCCATCATCAGCA----- 943
Db 2169 TGATGATCCCAATCTCCCATCATCAGCAAGGTACTACACATTTACATTTTTCATCATCGT 2228
QY 944 ----- 943
Db 2229 TTTTATCATACCATAGATATTTAAATGATTCATCATTTGCACCACATTAAGATATTCATC 2288
QY 944 -----AGG 946
Db 2289 ATCATCATCGTTACATTTTCTTGTGATCTTATGCTTCTCATATCTACTATTGTGTAGG 2348
QY 947 TTATTGACACATTAACGAAACATTAAGTTACTTCCCGGGTTCATATCAATGCACGACG 1006
Db 2349 TTATTGACACATTAACGAAACATTAAGTTACTTCCCGGGTTCATATCAATGCACGACG 2408
QY 1007 TGGCCTACTTTCGATTTCTTGAACCGGTGATCATGTGGAAGAAATAAACTCAGATCTTTGG 1066
Db 2409 TGGCCTACTTTCGATTTCTTGAACCGGTGATCATGTGGAAGAAATAAACTCAGATCTTTGG 2468
QY 1067 GATTATGGGAACCTTCTCATCTCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTTCTCG 1126
Db 2469 GATTATGGGAACCTTCTCATCTCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTTCTCG 2528
QY 1127 ATTTTCATAACCGGTGTGTCAAAGACATTTCTTCTTAAGCAAAATCAGCTTCGGGACTCG 1186
Db 2529 ATTTTCATAACCGGTGTGTCAAAGACATTTCTTCTTAAGCAAAATCAGCTTCGGGACTCG 2588
QY 1187 CTCTTCTCTATCCAAACACCGGAATA----- 1214
Db 2589 CTCTTCTCTATCCAAACACCGGAATAAGTACATCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 2648
QY 1215 -----ATGGGACAA 1223
Db 2649 AAGAACCAAGTAATAAATTTCTATGAACCTGATTATGCTGTTATTGTTAGATGGGACAA 2708
QY 1224 TCGTATGTGGCGGATGATACAGAGATCGATGAAGATGTTATATATATTTATCGGACTACT 1283
Db 2709 TCGTATGTGGCGGATGATACAGAGATCGATGAAGATGTTATATATATTTATCGGACTACT 2768
QY 1284 ACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAGAGCGTTAACGAGAGATAAATTAG 1343
Db 2769 ACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAGAGCGTTAACGAGAGATAAATTAG 2828
QY 1344 GTTTTGCAGGATTCAGGTATTAAAGATTAAGCAATATCTAATGCATTATCTAGTAAAGA 1403
Db 2829 GTTTTGCAGGATTCAGGTATTAAAGATTAAGCAATATCTAATGCATTATCTAGTAAAGA 2888
QY 1404 AGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAAGAGGAAAGATCTATT 1463
Db 2889 AGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAAGAGGAAAGATCTATT 2948
QY 1464 TGATCCCAAGAAACTGTTATCTCCAGGCGCAAGACATCTTTTGA 1506
Db 2949 TGATCCCAAGAAACTGTTATCTCCAGGCGCAAGACATCTTTTGA 2991

Db 716 AACTTGAAGTAGCTCCGAAAAGGGCCAAAGTGGTTAAGGTTTCTATACATAGATTCTCCG 775
 QY 725 CTTTACAAAGGACCAAGAACGTTTGTATATCAATGGCAACAGATATTGGAGTC---GACT 781
 Db 776 AATTCAAGAGATCAAGAACGAGTGAATATCGAAACGGACGGGTAGATTCTTTAGAA 835
 QY 782 ATTGAAGGTCATATTTCTATCAAAACGGTGTCTGTTGACACCTCTTTTCCACCTT 841
 Db 836 GTTCCATTATGGTGGACCATGGCCCAACCGGATAACTGGAGATCCACGTATTATCCAC 895
 QY 842 CAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGA 901
 Db 896 CCGATCACTTGAGGATCGCCTCAATGGTCAACGACATCGTGTATCTACTGCTCCITGA 955
 QY 902 TAGCCAAAGTATTATGATGATCCCAATCTCCCAATCATCAGCAAGGTTATTGACATTA 961
 Db 956 TCGTCAAGTATTACGACGAAACTTCTCAATACACAGTCAACGAGGAAATGGAGGATTA 1015
 QY 962 CGAAACATTAAGTACTTTCGCGGGTTGATATCAATGACGACGTGGCTTACTTCTGATT 1021
 Db 1016 GCGATAGTTTAAACCATGTAAGAGGGTTTATGTACGAGAAAGATGTGACGTATATG 1075
 QY 1022 TCTTGAACCGTGTATGATGATCCCAATCTCCCAATCATCAGATCTTTGGGATTATGG 1081
 Db 1076 TCCTAAACCGAGTTCGAACCGGAGAGCTAAACCTGAAATCCAAAGCCCAATGGGAT 1135
 QY 1082 CTCATCCTTGGCTTAACCTCTACGTTCTCTTAAATCTCGGATTCTCGATTCTTCAAT 1141
 Db 1136 CACATCCATGGCTTAATCTCTTGTACCAAAACTCAATCTCCAAATTTGATGATGGTG 1195
 QY 1142 TTGTCAAAGACATTTCTTTAAGCAAAATCAGCTTCGGGACTCGCTCTTCTCTATCAA 1201
 Db 1196 TTTTAAAGGGTATTATCTTAAGAAATAACATCACTAGCGGTCTCTTCTTGTATCTA 1255
 QY 1202 CAAACCGGAATAAATGGGACAATCGTATGTCGGGATGATACAGAGATCGATGAAGAT 1261
 Db 1256 TGAATCGCAACAAGTGAATGATCGGATGTCTGCCGTATATCCCGAG-----GA 1309
 QY 1262 TTATATATATTATCGSACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAGTGA 1321
 Db 1310 TATTTATGCGGTAGGTTTAAAGATCCGCGGTTTGTGACAAATGGGAGGCTTTTGA 1369
 QY 1322 GCGTTAAGGAGAAATAATAGGTTTTCGAAGGATTCAGGTTATTAAGATTAAAGCAAT 1381
 Db 1370 AAGAAACATGGAATACTGAAGTTTGTGAGGATGCTAATATGGGGTTTATACAAAT 1429
 QY 1382 TAATGCATTATACATAAGAAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATT 1441
 Db 1430 TTCCTTATCATTCACAAAGAGGATGGGTAGACATTTTGTGCTCCGAGGTGGAATAT 1489
 QY 1442 TTTGGAAGGAGAAAGATCTATTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACAT 1501
 Db 1490 TCGTAGAGAGAAATATAAATATGATCCCAAAATGATATTATCACCGGGACAAATAT 1549
 QY 1502 TT 1503
 Db 1550 TT 1551

RESULT 13
 US-10-014-101-27
 ; Sequence 27, Application US/10014101
 ; Publication No. US20030074698A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schumling, Thomas
 ; APPLICANT: Werner, Tom S
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and physiology
 ; FILE REFERENCE: 1195-2
 ; CURRENT APPLICATION NUMBER: US/10/014,101
 ; CURRENT FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833
 ; PRIOR FILING DATE: 2001-06-16

; PRIOR APPLICATION NUMBER: EP 00870132.8
 ; PRIOR FILING DATE: 2000-06-16
 ; PRIOR APPLICATION NUMBER: US 60/258,415
 ; PRIOR FILING DATE: 2000-12-27
 ; PRIOR APPLICATION NUMBER: EP 01870053.4
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 1572
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-10-014-101-27

Query Match 31.2%; Score 470; DB 14; Length 1572;
 Best Local Similarity 58.7%; Pred. No. 2.9e-130;
 Matches 881; Conservative 0; Mismatches 600; Indels 21; Gaps 3;
 QY 17 TAATGATCACTTTAATCAGGTTTAAATGATCACCATAATCATCAACCGGTATTAATTTG 76
 Db 56 TCATCATTAATCTCTCAACTCCGATCACAACCAACATCACCAACCATGGAATATCC 115
 QY 77 ATTACCTAAATCCCTTAACCTCACCTCTCTACCGATCTCTTCCATCATCTCCGAGCCT 136
 Db 116 TTTACACAAACGAATTCGCGGAAACTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 175
 QY 137 CTGATGACTTCGGAACATACACACCGTACCCCGGCGGCGGTAAATCTGCCCCCTCTCCA 196
 Db 176 CCACAGATTTCCGCGCCAGTCACCAAAATCTTCCCTTCCGCGGTCTTAATCCCTCTCC 235
 QY 197 CCGTGTATCT 256
 Db 236 TTGAAGACATCACAGATCTCATAAACTCTCTTTGACTCTCAACTGTCTCTCTCTCT 295
 QY 257 CCGTCTGTGGCCCAAGCCACTCTTAAACCGGCAAGCCCTCGGTCTCCGCGGAGTAATCG 316
 Db 296 CCGTCTGTGGTACGACACACAGCCACCGTGGCCAGCCCTCGGCTAAAGACGGAGTTGG 355
 QY 317 TCAACATGACGTGTATCACTGACGTGG-----TGGTTCAAAAGACAAAGAAGT 364
 Db 356 TCAACATGCGGTCCATGGTAAACCGGGATCGAGGTATCAAGGTGTCTAGGACCTGTTAT 415
 QY 365 ACGTGTGCGGCGCGGACGTTTATGGGTGATGTCTTAAAGACACGGCGGAGAAAG 424
 Db 416 ATGTGACGTGGACGCTGCGTGGCTATGGATGAGGTGTGAATAAACTTTGGAGTTAG 475
 QY 425 GGGTGTGCGCGGTTTCTTGGACGGATTATTTGCATATAACCGTCCGAGGAACTGTCGA 484
 Db 476 GGTAAACGCGGTTTCTTGGACGGATTATTTGTATTTAAACAGTCGTTGGGACGTTATCAA 535
 QY 485 ATGTGGAATTGGTGTCAAGTGTTCGAAACGGTCTCTTGTGTAGTAACGTTCTTGAAT 544
 Db 536 ACGCGGAATTAGTGGACAAACGTTTCCGTACGGTCCACAGATCACTAATGTTCTAGAGA 595
 QY 545 TGGACGTATTACTGGGAAAGGTGAAATGTTGACATGCTCGGACACGCTAAACCCAGAA 604
 Db 596 TGGATGTTATTACTGGGAAAGGAGAGATTGCAACTTGTTCGAAGGACATGAACCTCGGATC 655
 QY 605 TGTCTATGGAGTTTAGGAGTTTGGGTCAATTTGGAATTATTAACGAGAGCCAGAAATTG 664
 Db 656 TTTTCTTCCGCGTGTAGGAGGTTTGGGTCAATTCGGCATTTATAACAGAGCCAGAAATTA 715
 QY 665 TTTTGGACCATGCACCTAAACGGGCAAAATGTTTGGATGCTCTACAGTGAATTCACAA 724
 Db 716 AACTTGAAGTAGCTCCGAAAGGGCCAAAGTGTAAAGTTTCTATACATAGATTCTCCG 775
 QY 725 CTTTACAAAGGACCAAGAACGTTTGTATATCAATGGAACGCAATATGGAGTC---GACT 781
 Db 776 AATTCAAGAGATCAAGAACGAGTGAATATCGAAACCGGACGGGTGTAGATTCTTTAGAG 835
 QY 782 ATTTAGAAGGTCAAAATATTCTATCAACCGGTGTGTTGACACCTCTTTTCCACCTT 841
 Db 836 GTTCCATTATGGTGGACCATGGCCCAACCGGATAACTGGAGATCCACGTATTATCCACCGT 895

QY 842 CAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAG 901
DB 896 CCGATCACTTGAGGATCGCCTCAATGGTCAAAACGACATCGTGTCTACTGCTTGAAG 955
QY 902 TAGCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTAA 961
DB 956 TCGTCAAGTATTACGACGAACTTCTCAATACACAGTCAACGAGGAAATGGAGAGTTAA 1015
QY 962 CGAAACATTAAGTTACTTGGCCGGTTTCATATCAATGACAGACGTGGCCTACTTCGATT 1021
DB 1016 GCGATAGTTTAAACCATGTAAAGGGTTTATGTACGAGAAAGATGTGACGTATATGGATT 1075
QY 1022 TCCTGAACCGTGTACATGTCGAAGAAAATAAACTCAGATCTTTGGGATTATGGGAATTC 1081
DB 1076 TCCTAAACCGAGTTCGAACCCGGAGAGCTAAACCTGAAATCCAAAGGCCAATGGGATGTT 1135
QY 1082 CTCATCCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATCTCTCGATTTCATACGGTG 1141
DB 1136 CACATCCATGGCTTAATCTCTTCGTACCAAAAACCTCAATCTCCAAATTTGATGATGGTG 1195
QY 1142 TTGTCAAGACATTTCTTAAAGCAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCAA 1201
DB 1196 TTTTAAAGGTATTATCTTAAGAAATAACATCACTAGCGGTCTGTTCTTGTATTCTTA 1255
QY 1202 CAAACCGGAATAAATGGGACAATCGTATGTGCGCGATGATACAGAGATCGATGAAGATG 1261
DB 1256 TGAATCGCAACAAGTGGAAATGATCGGATGTCTGCCGCTATACCCGAG-----GAAGATG 1309
QY 1262 TTATATATATATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAGA 1321
DB 1310 TATTTTATGCGGTAGGGTTTTTAAAGATCCGCGGGTTTTTGACAAATGGGAGGCTTTTGATC 1369
QY 1322 GCGTTAACGAGAAGATAATTAGTTTTCGAAGGATTCAGGTATTAAAGATTAAAGCAATATC 1381
DB 1370 AAGAAACATGGAATACTGAAGTTTGTGAGGATGCTAATATGGGGTTATACAATATC 1429
QY 1382 TAATGCATTATAGTAAAGAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATT 1441
DB 1430 TTCTTTATCATTATCATCAAGAAGGATGGGTTAGACATTTTGGTCCGAGGTGGAATATT 1489
QY 1442 TTTCGAAGAGGAAAGATCTATTTGTATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCT 1501
DB 1490 TCGTAGAGAGAAAATATAAATATGATCCCAAAATGATATTATACCCGGGACAAAATATAT 1549
QY 1502 TT 1503
DB 1550 TT 1551

RESULT 14
US-10-326-184-9
; Sequence 9, Application US/10326184
; Publication No. US20030163847A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C
; TITLE OF INVENTION: OXIDASE 1
; FILE REFERENCE: MTC6781.1
; CURRENT APPLICATION NUMBER: US/10/326,184
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/343,129
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-326-184-9

Query Match 31.2%; Score 470; DB 14; Length 1572;
Best Local Similarity 58.7%; Pred. No. 2.9e-130;

Matches 881; Conservative 0; Mismatches 600; Indels 21; Gaps 3;
QY 17 TAATGATCACTTTAATCACGGTTTTAATGATCACCAAAATCATCAAAACGGTATTAAATTG 76
DB 56 TCATCATTAATCTCTCAACTCCGATCACAACCAACACATCACCACAACCATGGAATATCC 115
QY 77 ATTTACCTAAATCCCTTAAACCTCACCTCTCTAGCGATCCTTCCATCATCTCCGAGCCT 136
DB 116 TTTCACACAACGAATTGCGCCGGAATACTCACCTCCTCCTCCTCCTCGTCAATCAGCG 175
QY 137 CTCATGACTTCGGAACATAACACACCGTGACCCCGGGCGGTAATCTGCCCTCCTCCA 196
DB 176 CCACAGATTCGGCCACGTCACCAAAATCTTCCCTTCCGCGCTTAATCCCTTCCCTCG 235
QY 197 CCGCTGATATCTCTCGTCTCCTCCAATACCGCCGCAACCGGAAAAAGTACATTCGAAGTAG 256
DB 236 TTGAAGACATCACAGATCTCATAAAACTCTCTTTTGACTCTCAACTGTCTTTTCCCTTAG 295
QY 257 CCGCTCGTGGCCAAAGGCCACTCCTTAAACGGCCAAAGCCCTCGGTCTCCGGCGGAGTAATCG 316
DB 296 CCGCTCGTGTACGGACACAGCCACCGTGGCCAAAGCCCTCGGTAAGACGGAGTTGTGG 355
QY 317 TCAACATGACGTGTATCACTGACGTGG-----TGGTTTCAAAAGACAAGAAAT 364
DB 356 TCAACATGCGGTCCATGGTAAACCGGGATCGAGGTATCAAGGTGTCTAGGACCTGTTTAT 415
QY 365 ACGCTGACGTGGCGCGCGGACGTTATGGGTGGATGTGCTTAAAGACACGGCGGAGAAAG 424
DB 416 ATGTTGACGTGACGCTCGTGGCTATGGATTGAGGTGTTGAATAAAACTTTGGAGTTAG 475
QY 425 GGGTGTGCGCGGTTCTTGGACGGATTATTTGCATATAAACCCTCGGAGGAACGTTGTCTGA 484
DB 476 GGTAAACGCCCGGTTCTTGGACGGATTATTTGATTTAACAGTCGGTGGGACGTTATCAA 535
QY 485 ATGGTGAATTTGGTGGTCAAGTGTTCGAAACGGTCTCTTTGTAGTAACGTCCTTGAAT 544
DB 536 ACGCGGAATTAGTGGAACAAACGTTTCGGTACGGTCCACAGATCACTAATGTTCTTAGAGA 595
QY 545 TGGACGTTATTACTGGGAAAGGTGAATGTTGACATGCTCGGACAGCTAAACCCAGAAAT 604
DB 596 TGGATGTTATTACTGGAAGAGAGAGATTGCAACTTGTTCGAAGCATGAACCTCGGATC 655
QY 605 TGTTCTATGGAGTGTAGGAGGTTTGGGTCAATTTGGAATTTAAGAGAGCCAGAAATTG 664
DB 656 TTTTCTTCGCGGTGTAGGAGGTTTGGGTCAATTCGGCATTTAACAAGAGCCAGAAATTA 715
QY 665 TTTTGGACCATGCACTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGAATTTTCACAA 724
DB 716 AACTTGAAGTAGCTCCGAAAAGGGCCAAAGTGTAAAGTTTCTATACATAGATTTCTCCG 775
QY 725 CTTTACAAAAGGACCAAGAACGTTTGTATATCAATGGAACGCAACGATATTGGAGTC---GACT 781
DB 776 AATTCAACAAGAGATCAAGAACGAGTGATATCGAAAAACGGACGGTGTAGATTTCTTAGAAG 835
QY 782 ATTTAGAAGGTCAAATATTCTATCAAAACGGGTGTGTTGACACCTCTTTTTCACACCTT 841
DB 836 GTTCCATTATGGTGGACCATGGCCACCGGATAAATCGGAGATCCACGTATATCCACCGT 895
QY 842 CAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGCGTATCATCTATGTTCTTGAAG 901
DB 896 CCGATCACTTGAGGATCGCTCAATGGTCAAAACGACATCGTGTCTACTCTACTGCTTGAAG 955
QY 902 TAGCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTAA 961
DB 956 TCGTCAAGTATTACGACGAAACTTCTCAATACACAGTCAACGAGGAAATGGAGAGTTAA 1015
QY 962 CGAAAACATTAAAGTTACTTGGCCGGTTTCATATCAATGACAGACGTGGCCTACTTCGATT 1021
DB 1016 GCGATAGTTTAAACCATGTAAAGGGTTTATGTACGAGAAAGATGTGACGTATATGGATT 1075
QY 1022 TCCTGAACCGTGTACATGTGGAAGAAAATAAACTCAGATCTTTGGGATTATGGGAATTC 1081
DB 1076 TCCTAAACCGGAGTTTCGAACCGGAGAGCTAAACCTGAAATCCAAAGGCCAATGGGATGTT 1135

QY	1082	CTCATCCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTCCTCGATTTTCATTAACGGTG	1141
Db	1136	CACATCCATGGCTTAATCTCTTCGTACCAAAACTCAAATCTCCAAATTTGATGATGGTG	1195
QY	1142	TTGTCAAAGACATCTTCTTAAGCAAAATCAGCTTCGGGACTCGCTCTCTCTATCCAA	1201
Db	1196	TTTTTAAGGGTATATCTTAAGAAATAACATCACTAGCGGTCTCTTCTTGTATCCCTA	1255
QY	1202	CAAAACGGGAATAATGGGACAAATCGTATGTGGCGATGATACCAAGATCGATGAAGATG	1261
Db	1256	TGAATCGCAACAAGTGAATGATCGGATGTTCTGCCGTATACCCGAG-----GAAGATG	1309
QY	1262	TTATATATATATTCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAGTGGAGA	1321
Db	1310	TATTTATGCGGTAGGGTTTTTAAGATCCGCGGGTTTTTGACAAATGGGAGGCTTTTGATC	1369
QY	1322	GCGTTAACGAGAGAAATATAGGTTTTTGCAAGGATTCAGGTATTAAGATTAAGCAATATC	1381
Db	1370	AAGAAACATGGAATACTGAAGTTTTGTGAGGATGCTAATATGGGGTTATACAATATC	1429
QY	1382	TAATGCATTATACTAGTAAAGAAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATT	1441
Db	1430	TTCCCTTATCATTCATCAAGAAGGATGGTTTAGACATTTTGGTCCGAGGTGGAATATTT	1489
QY	1442	TTTCGAAGAGGAAAGATCTATTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCT	1501
Db	1490	TCGTAGAGAGAAAATATAAATATGATCCCAAAATGATATTATCACCGGACAAAATATAT	1549
QY	1502	TT 1503	
Db	1550	TT 1551	
RESULT 15			
US-10-311-453-29			
; Sequence 29, Application US/10311453			
; Publication No. US20040031073A1			
; GENERAL INFORMATION:			
; APPLICANT: Schmilling, Thomas			
; APPLICANT: Werner, Tom s			
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and			
; TITLE OF INVENTION: physiology			
; FILE REFERENCE: 1226-4			
; CURRENT APPLICATION NUMBER: US/10/311,453			
; CURRENT FILING DATE: 2002-12-16			
; PRIOR APPLICATION NUMBER: EP 00870132.8			
; PRIOR FILING DATE: 2000-06-16			
; PRIOR APPLICATION NUMBER: US 60/258,415			
; PRIOR FILING DATE: 2000-12-27			
; PRIOR APPLICATION NUMBER: EP 01870053.4			
; PRIOR FILING DATE: 2001-03-16			
; NUMBER OF SEQ ID NOS: 36			
; SOFTWARE: Patentin Ver. 2.1			
; SEQ ID NO 29			
; LENGTH: 1611			
; TYPE: DNA			
; ORGANISM: Arabidopsis thaliana			
US-10-311-453-29			
Query Match 20.3%; Score 306.2; DB 12; Length 1611;			
Best Local Similarity 53.6%; Pred. No. 6.6e-81;			
Matches 775; Conservative 0; Mismatches 628; Indels 42; Gaps 5;			
QY	95	ACCTCACCTCTCTACCGATCCTTCCATCATCTCCGACGCTCTCATGACTTCGGAAACA	154
Db	110	ACGGCCACTTCACCGTCCACCCCTTCGACTTAGCCTCCGCTCTCCTCAGACTTCGGTATGC	169
QY	155	TAA---CCACGTGACCCCGCGGGCGTAATCTGCCCTCTCTCCACCGCTGATATCTCTC	211
Db	170	TGAAGTCACCTGAAGAGCCATTGGCCGTGCTTCATCCATCATCGGCCGAAGACGTGGCAC	229
QY	212	GTCTCCTCCATACGCGCAACGGAAGAAAGTACATTCCAAGTAGCGGCTCGTGGCCAAG	271
Db	230	GACTCGTCAGAACAGCTTACGGTTACGCCACGGCTTTCGGTCTCAGCCCAGGCCACG	289
QY	272	GCCACTCCTTAAACGGCCAAGCCTCG-----GTCTCCGGCGGAGTAATCG	316
Db	290	GCCATTCCATAAACGACAAAGCCGCGGGGAGGAACGGTGTGCTGTTGAAATGAACC	349
QY	317	TCAACATGACGTGTATCACTGACGTGTGTGGTTTCAAAAGACAAGAGTACGCTGACGTGG	376
Db	350	ACGGCGTAACCCGGACGCCAAGCCACTCGTCCGACCGGATGAATGTATGTGGATGTAT	409
QY	377	CGGCCGGGACGTTATGGGTGGATGTGCTTAAGAAAGACGGCGGAGAAAGGGGTGTCCCGG	436
Db	410	GGGGTGGAGAGTTATGGGTGATGTGTTGAAGAAAAACGTTGGAGCATGGCTTAGCACCAA	469
QY	437	TTTCTTGGACGGATTAATTTGCATATAACCGTCGGAGGAACGTTGTGCAATGGTGAATTG	496
Db	470	AATCATGGACGGATTACTTGATCTAACCGTTGGAGGTACACTCTCCAATGCAGGAATCA	529
QY	497	GTGGTCAAGTGTTCGAAAACGGTCCCTCTTGTAGTAACGTCCTTGAATGGACGTTATTA	556
Db	530	GTGGTCAAGCTTTTCACCATGGTCTCAAAATAGTAACGTCCTTGAGCTCGACGTTGTAA	589
QY	557	CTGGAAAGGTGAATGTGACATGCTCGCGACAGCTAAACCCAGAAATTTCTATGGAG	616
Db	590	CTGGAAAGGAGAGGTGATGAGATGCTCAGAAAGAGAGAACACAAAGGCTATTCATGGAG	649
QY	617	TGTTAGGAGGTTTGGGTCAATTTGGAATTAACGAGAGCCAGAAATTTGTTGGACCATG	676
Db	650	TTCTTGGTGGATTAGGTCAATTTGGGATCATCACTCGAGCACGAATCTCTCTCGAACCA	709
QY	677	CACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGATTTCAACAACITTTTACAAAG	736
Db	710	CTCCCCAAAGGTGAGATGGATACGGGTATTGTATTGAGCTTCAAAGTGTTCACGGAGG	769
QY	737	ACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGACTATTTAGAAAGGTCAAA	796
Db	770	ACCAAGAGTACTTAATCTCAATGCATGGTCAATTAAGATTGATTACGTGGAAGGTTTG	829
QY	797	TATTTCTATCAACCGGTGCTTGACA-----CCTCTTTTCCACCTTCAGATC	847
Db	830	TGATTGTGGACGAAGGACTCGTCAACAATTTGGAGATCTTCTTCTCTCCACGTAACC	889
QY	848	AATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTTGAAGTAGCCA	907
Db	890	CCGTCAAGATCTCCTCTGTAGTTCACACGGCTCTGTTGTATTGCCCTTGAGATCACCA	949
QY	908	AGTATTATGATGATCCCAATCTCCCCATCATCAGCAAGGTTATTGACACATTAAACGAAAA	967
Db	950	AGAACTACCACGACTCCGACTCCGAAATCGTTGATCAGGAAGTTGAGATCTCTGATGAAGA	1009
QY	968	CATTAAAGTTACTTGCCCGGTTTCATATCAATGCACGACGTGGCCTACTTCGATTCTTGA	1027
Db	1010	AATTGAATTTCATACCGACATCGGTCTTTTACAACGGATTTACAATATGTGGACITTTCTG	1069
QY	1028	ACCGTGTACATGTCGAAGAAAAATAAACTCAGATCTTTGGATTATGGGAACITTCCTCATC	1087
Db	1070	ACCGGTACACAAGGCCGAATTGAAGCTCCGTTCCAAAGAAATTTATGGAGGTTCCACACC	1129
QY	1088	CTTGGCTTAACCTCTACGTTCTTAAATCTCGGATTCTCGATTTTCATAACGGTGTGTGCA	1147
Db	1130	CATGGCTCAACCTCTTCGTGCCAAAAATCAAGAAATCTCTGACTTCGATAAAGCGTTTTC	1189
QY	1148	AAGACATTTCTTTAAGCAAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCAAACAACC	1207
Db	1190	AGGGCATTTTGGGAAATAAAACAA-----GTGGCCCTATTCTTACTACCCCATGAACA	1243
QY	1208	GGAATAAATGGGACAAATCGTATGTGCGCGATGATACC-----AGAGATCGATGAAG	1258
Db	1244	AAGACAAATGGGACGAGAGGAGCTCAGCCGTGACGCCGGATGAGGAAGTTTCTATCTGG	1303
QY	1259	ATGTTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAAAGTGG	1318

Db	1304	TGGCTCTATTGAGATCAGCTTTAAACGGACGGTGAAGAGACACAGAAGCTAGAGTATCTGA	1363
QY	1319	AGAGCGTTAACGAGAGATAATTAGGTTTTGCCAAGGATTTCAGGTATTAAAGATTAAAGCAAT	1378
Db	1364	AAGATCAGAAACCGTCGGATCTTGGAGTTCTGTGAACAAGCCAAAGATCAATGTGAAGCAGT	1423
QY	1379	ATCTAATGCATTATATACTAGTAAAGAAGATTGGATTGAGCATTTTGGATCAAAATCGGATG	1438
Db	1424	ATCTTCCTCACCACGCAACACAGAGAAGAGTGGGTGGCTCATTTTGGGGACAAAGTGGGATC	1483
QY	1439	ATTTTTCGAAGAGGAAAGATCTATTGATCCCAAGAACTGTTATCTCCAGGGCAAGACA	1498
Db	1484	GGTTCAGAAGCTTAAAGGCTGAGTTTGATCCGCGACACATACTCGCTACTGGTCAAGAA	1543
QY	1499	TCCTT	1503
Db	1544	TCCTT	1548

Search completed: April 7, 2004, 07:46:10
Job time : 620 secs

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OM protein - protein search, using sw model

Run on: April 5, 2004, 17:37:46 ; Search time 59 Seconds
(without alignments)
2399.259 Million cell updates/sec

Title: US-10-014-101-4
Perfect score: 2596
Sequence: 1 MANLRMITLITVLMITKSS.....SKRKDLFDPKLLSPGQDIF 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2596	100.0	501	5 AAU81968	Aau81968 A. thalia
2	2596	100.0	501	6 ABR63565	Abr63565 Arabidops
3	2596	100.0	501	6 ABR63569	Abr63569 Arabidops
4	2579	99.3	515	3 AAG31940	Aag31940 Arabidops
5	2579	99.3	515	5 ABB91811	Abb91811 Arabidops
6	2551	98.3	509	3 AAG31941	Aag31941 Arabidops
7	2516	96.9	501	3 AAG31942	Aag31942 Arabidops
8	1822	70.2	524	3 AAG31316	Aag31316 Arabidops
9	1822	70.2	524	5 ABB93161	Abb93161 Arabidops
10	1822	70.2	524	5 AAU81970	Aau81970 A. thalia
11	1822	70.2	524	6 ABR63567	Abr63567 Arabidops
12	1822	70.2	524	6 ABR63571	Abr63571 Arabidops
13	1511.5	58.2	400	3 AAG31317	Aag31317 Arabidops
14	1505.5	58.0	395	3 AAG31318	Aag31318 Arabidops
15	1292	49.8	523	5 ABB93847	Abb93847 Arabidops
16	1292	49.8	523	5 AAU81969	Aau81969 A. thalia
17	1292	49.8	523	6 ABR63566	Abr63566 Arabidops
18	1292	49.8	523	6 ABR63570	Abr63570 Arabidops
19	1184	45.6	536	5 ABB91608	Abb91608 Arabidops
20	1184	45.6	536	5 AAU81971	Aau81971 A. thalia
21	1184	45.6	536	6 ABR63572	Abr63572 Arabidops
22	1184	45.6	539	5 AAU81974	Aau81974 A. thalia
23	1184	45.6	539	6 ABR63575	Abr63575 Arabidops
24	1141.5	44.0	535	3 AAB30691	Aab30691 Amino aci
25	1141	44.0	534	2 AAW93007	Aaw93007 Z. mays c

26	1141	44.0	534	6 ABR63563	Abr63563 Maize cyt
27	1126.5	43.4	611	5 AAU81968	Aae13725 pJE-7 pla
28	1056.5	40.7	575	5 ABB92071	Abb92071 Herbicida
29	1056.5	40.7	575	5 AAU81967	Aau81967 A. thalia
30	1056.5	40.7	575	6 ABR63568	Abr63568 Arabidops
31	1056.5	40.7	575	6 ABR63564	Abr63564 Arabidops
32	993	38.3	504	5 ABB92780	Abb92780 Herbicida
33	993	38.3	504	5 AAU81972	Aau81972 A. thalia
34	993	38.3	504	6 ABR63573	Abr63573 Arabidops
35	557	21.5	113	3 AAG15003	Aag15003 Arabidops
36	457	17.6	487	6 ABJ37455	Abj37455 Benzodiaz
37	363	14.0	72	3 AAG15004	Aag15004 Arabidops
38	226.5	8.7	515	4 AAG90381	Aag90381 C glutami
39	207.5	8.0	476	6 ABM70602	Abm70602 Photorhab
40	193.5	7.5	495	2 AAY24919	Aay24919 Microdoch
41	188	7.2	544	4 AAB81081	Aab81081 Cannabidi
42	183.5	7.1	459	7 ADB74298	Adb74298 Mycobacte
43	178	6.9	472	3 AAB32526	Aab32526 S. lavend
44	178	6.9	472	7 ADE10298	Adel0298 S. lavend
45	178	6.9	488	4 AAB80058	Aab80058 Corynebac

ALIGNMENTS

RESULT 1
AAU81968
ID AAU81968 standard; protein; 501 AA.
XX
AC AAU81968;
XX
DT 09-APR-2002 (first entry)
XX
DE A. thaliana cytokinin oxidase AtCKX2.
XX
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarpy.
XX
OS Arabidopsis thaliana.
XX
PN WO200196580-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-EP006833.
XX
PR 16-JUN-2000; 2000EP-00870132.
PR 27-DEC-2000; 2000US-0258415P.
PR 16-MAR-2001; 2001EP-00870053.
(SCHEM/) SCHMULLING T.
(WERN/) WERNER T.
Schmulling T, Werner T;
WPI; 2002-130736/17.
N-PSDB; ABK28607.

Polynucleotide encoding novel plant protein having cytokinin oxidase activity and the protein useful for stimulating root growth, enhancing the formation of lateral or adventitious roots, altering root geotropism.

Claim 12; Page 129-131; 154pp; English.

The invention relates to an isolated polynucleotide (I) encoding a novel plant protein (II) having cytokinin oxidase activity. (I) is useful for production of transgenic plants, plant cells or tissues; for production of altered plants, plant cell or tissues; and for effecting the expression of (II) where (I) is operably linked to one or more control sequences. The methods further comprises regenerating a plant from the plant cell. (I) and (II) are useful for stimulating root growth; enhancing the formation of lateral or adventitious roots; altering root

CC geotropism, leading to an increase in yield; and for screening growth
 CC promoting chemical of herbicides. (I) is useful for increasing the size
 CC of the root meristem; increasing root size; increasing the size of the
 CC shoot meristem; delaying leaf senescence and altering leaf senescence;
 CC increasing leaf thickness; reducing or increasing the vessel size;
 CC inducing parthenocarp; improving standability of the seedlings;
 CC increasing branching and for improving lodging resistance. Antibody (III)
 CC to (II) is useful for identifying and obtaining proteins interacting with
 CC (II) comprising a screening assay, preferably a two-hybrid screening
 CC assay. AAU81967-AAU81974 represent Arabidopsis thaliana cytokinin oxidase
 CC amino acid sequences
 XX
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2596; DB 5; Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.2e-234;
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTPGGV 60
 DB 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTPGGV 60
 QY 61 ICPSTADISRLLOAANGKSTFQVAARGQSHSLNGQASVSGGVVNMTCITDVVYSKDK 120
 DB 61 ICPSTADISRLLOAANGKSTFQVAARGQSHSLNGQASVSGGVVNMTCITDVVYSKDK 120
 QY 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYHITVGGTSLNGGIGGVFRNGPLVSNVL 180
 DB 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYHITVGGTSLNGGIGGVFRNGPLVSNVL 180
 QY 181 ELDVITKGEMLTCSRQNLNPELFYGVGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
 DB 181 ELDVITKGEMLTCSRQNLNPELFYGVGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
 QY 241 TTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
 DB 241 TTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
 QY 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLRSLGLWEL 360
 DB 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLRSLGLWEL 360
 QY 361 PHPWNLVYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWNRMSAMIPEIDED 420
 DB 361 PHPWNLVYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWNRMSAMIPEIDED 420
 QY 421 VIYIIGLLQSATPKDLPEVESVNEKIIIRFCDSGKIKIKQYLMHYTSKEDWIEHFGSKWDD 480
 DB 421 VIYIIGLLQSATPKDLPEVESVNEKIIIRFCDSGKIKIKQYLMHYTSKEDWIEHFGSKWDD 480
 QY 481 FSKRKDLFDPKLLSPGQDIF 501
 DB 481 FSKRKDLFDPKLLSPGQDIF 501

RESULT 2
 ABR63565
 ID ABR63565 standard; protein; 501 AA.
 XX
 AC ABR63565;
 XX
 DT 18-SEP-2003 (first entry)
 XX
 DE Arabidopsis cytokinin oxidase AtCKX2.
 XX
 KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
 KW embryo size; cotyledon size; transgenic plant; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO2003050287-A2.
 XX
 PD 19-JUN-2003.

XX 10-DEC-2002; 2002WO-EP013990.
 PF 10-DEC-2001; 2001US-00014101.
 PR (SCHM/) SCHMULLING T.
 PA (WERN/) WERNER T.
 XX Schmulling T, Werner T;
 PI WPI; 2003-541577/51.
 XX
 PT Stimulating root growth, enhancing lateral or adventitious root formation
 PT or altering root geotropism comprises increasing plant cytokinin oxidase
 PT levels or other protein or nucleic acid that reduces active cytokinins in
 PT a plant.
 XX Example 2; Fig 2; 177pp; English.

PS The present invention relates to a method for stimulating root growth or
 XX enhancing the formation of lateral or adventitious roots or altering root
 CC geotropism, which comprises increasing in a plant or plant part the level
 CC of a plant cytokinin oxidase or other protein that reduces the level of
 CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
 CC coding sequences from Arabidopsis thaliana are also provided. The method
 CC is useful in modifying plant morphological, biochemical and physiological
 CC properties, such as in modifying the initiation, stimulation or
 CC enhancement of root growth, adventitious root formation, lateral root
 CC formation, root geotropism, shoot growth, apical dominance, branching,
 CC timing of senescence, timing of flowering, flower formation, seed
 CC development and/or seed yield. The present sequence is a protein shown in
 CC the invention
 XX Sequence 501 AA;

Query Match 100.0%; Score 2596; DB 6; Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.2e-234;
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTPGGV 60
 DB 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTPGGV 60
 QY 61 ICPSTADISRLLOAANGKSTFQVAARGQSHSLNGQASVSGGVVNMTCITDVVYSKDK 120
 DB 61 ICPSTADISRLLOAANGKSTFQVAARGQSHSLNGQASVSGGVVNMTCITDVVYSKDK 120
 QY 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYHITVGGTSLNGGIGGVFRNGPLVSNVL 180
 DB 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYHITVGGTSLNGGIGGVFRNGPLVSNVL 180
 QY 181 ELDVITKGEMLTCSRQNLNPELFYGVGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
 DB 181 ELDVITKGEMLTCSRQNLNPELFYGVGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
 QY 241 TTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
 DB 241 TTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
 QY 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLRSLGLWEL 360
 DB 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLRSLGLWEL 360
 QY 361 PHPWNLVYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWNRMSAMIPEIDED 420
 DB 361 PHPWNLVYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWNRMSAMIPEIDED 420
 QY 421 VIYIIGLLQSATPKDLPEVESVNEKIIIRFCDSGKIKIKQYLMHYTSKEDWIEHFGSKWDD 480
 DB 421 VIYIIGLLQSATPKDLPEVESVNEKIIIRFCDSGKIKIKQYLMHYTSKEDWIEHFGSKWDD 480
 QY 481 FSKRKDLFDPKLLSPGQDIF 501
 DB 481 FSKRKDLFDPKLLSPGQDIF 501

Db 481 FSKRKDLFDPKKLLSPGQDIF 501

RESULT 3

ABR63569
ID ABR63569 standard; protein; 501 AA.
XX

AC ABR63569;

DT 18-SEP-2003 (first entry)

XX Arabidopsis cytokinin oxidase-like protein 2.

DE
XX
XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide.
KW

OS Arabidopsis thaliana.

XX
XX
PN WO2003050287-A2.

XX
PD 19-JUN-2003.

XX
PF 10-DEC-2002; 2002WO-EP013990.

XX
PR 10-DEC-2001; 2001US-00014101.

XX (SCHM/) SCHMULLING T.
PA (WERN/) WERNER T.

XX
PI Schmullling T, Werner T;

XX
DR WPI; 2003-541577/51.
DR N-PSDB; ACC85276.

XX
PT Stimulating root growth, enhancing lateral or adventitious root formation
PT or altering root geotropism comprises increasing plant cytokinin oxidase
PT levels or other protein or nucleic acid that reduces active cytokinins in
PT a plant.

XX
PS Claim 19; Page 146-148; 177pp; English.

XX
CC The present invention relates to a method for stimulating root growth or
CC enhancing the formation of lateral or adventitious roots or altering root
CC geotropism, which comprises increasing in a plant or plant part the level
CC of a plant cytokinin oxidase or other protein that reduces the level of
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and
CC coding sequences from Arabidopsis thaliana are also provided. The method
CC is useful in modifying plant morphological, biochemical and physiological
CC properties, such as in modifying the initiation, stimulation or
CC enhancement of root growth, adventitious root formation, lateral root
CC formation, root geotropism, shoot growth, apical dominance, branching,
CC timing of senescence, timing of flowering, flower formation, seed
CC development and/or seed yield. The present sequence is a protein shown in
CC the invention

XX
SQ Sequence 501 AA;

Query Match 100.0%; Score 2596; DB 6; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.2e-234;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLRMITLITVLMITKSSNGIKIDLPKSLNLTLDPSIIISAASHDFGNITVTTPGGV 60
Db 1 MANLRMITLITVLMITKSSNGIKIDLPKSLNLTLDPSIIISAASHDFGNITVTTPGGV 60

QY 61 ICPSSSTADISRLQLYAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCTDWWVSKDK 120
Db 61 ICPSSSTADISRLQLYAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCTDWWVSKDK 120

QY 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGQVFRNGPLVSNVL 180
Db 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGQVFRNGPLVSNVL 180

QY 181 ELDVITGKGEMLTCSRQLNPFLFYGLGGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 ELDVITGKGEMLTCSRQLNPFLFYGLGGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
QY 241 TTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSPQSKVADLVKQHGIYYVLE 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 TTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSPQSKVADLVKQHGIYYVLE 300
QY 301 VAKYYDDPNLPIISKVIDTLTKTLSYLPGFISMHDVAYFDFLNRVHVEENKLRSLGLWEL 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 VAKYYDDPNLPIISKVIDTLTKTLSYLPGFISMHDVAYFDFLNRVHVEENKLRSLGLWEL 360
QY 361 PHPWLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPNTNRNKWDNRMSAMIDEID 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 PHPWLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPNTNRNKWDNRMSAMIDEID 420
QY 421 VIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGKIKQYLMHYTSKEDWIEHFGSKWDD 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 VIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGKIKQYLMHYTSKEDWIEHFGSKWDD 480
QY 481 FSKRKDLFDPKKLLSPGQDIF 501
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 FSKRKDLFDPKKLLSPGQDIF 501

RESULT 4

AAG31940
ID AAG31940 standard; protein; 515 AA.

XX
AC AAG31940;

XX
DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 38444.

DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX
PN EP1033405-A2.

XX
PD 06-SEP-2000.

XX
PF 25-FEB-2000; 2000EP-00301439.

XX
PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 99.3%; Score 2579; DB 3; Length 515;
Best Local Similarity 97.3%; Pred. No. 5e-233;
Matches 501; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

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|||
Db 1 MANRLMITLITVLMITKSSNGIKIDLPKSLNLTLDPSIISAASHDFGNITVTPGGV 60
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QY 61 ICPSSTADISRLQLQYAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCTITDVVVSXDK 120
|||
Db 61 ICPSSTADISRLQLQYAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCTITDVVVSXDK 120
|||

QY 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLVSNVL 180
|||
Db 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLVSNVL 180
|||

QY 181 ELDVITKGEMLTCSRQLNPFLFYGLGGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
|||
Db 181 ELDVITKGEMLTCSRQLNPFLFYGLGGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
|||

QY 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSPFPSPDQSKVADLVKQHGIIYVLE 300
|||
Db 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSPFPSPDQSKVADLVKQHGIIYVLE 300
|||

QY 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLRSLGLWEL 360
|||
Db 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLRSLGLWEL 360
|||

QY 361 PHPWNLVVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRN-----KW 406
|||
Db 361 PHPWNLVVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKYILLFIHIYLOEPKW 420
|||

QY 407 DNRMSAMIPEDIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGIIKQYLMHYTS 466
|||
Db 421 DNRMSAMIPEDIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGIIKQYLMHYTS 480
|||

QY 467 KEDWIEHFGSKWDDFSKRKDLFDPKLLSPGQDIF 501
|||
Db 481 KEDWIEHFGSKWDDFSKRKDLFDPKLLSPGQDIF 515
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RESULT 5
ABB91811
ID ABB91811 standard; protein; 515 AA.
XX
AC ABB91811;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 1022.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP009892.
XX
PR 28-AUG-2001; 2001WO-EP009892.
XX
PA (FARB) BAYER AG.

XX Tietjen K, Weidler M;
XX WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX
PS Claim 5; SEQ ID NO 1022; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides
XX
SQ Sequence 515 AA;
Query Match 99.3%; Score 2579; DB 5; Length 515;
Best Local Similarity 97.3%; Pred. No. 5e-233;
Matches 501; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MANRLMITLITVLMITKSSNGIKIDLPKSLNLTLDPSIISAASHDFGNITVTPGGV 60
|||
Db 1 MANRLMITLITVLMITKSSNGIKIDLPKSLNLTLDPSIISAASHDFGNITVTPGGV 60
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QY 61 ICPSSTADISRLQLQYAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCTITDVVVSXDK 120
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Db 61 ICPSSTADISRLQLQYAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCTITDVVVSXDK 120
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QY 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLVSNVL 180
|||
Db 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLVSNVL 180
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QY 181 ELDVITKGEMLTCSRQLNPFLFYGLGGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
|||
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|||
Db 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSPFPSPDQSKVADLVKQHGIIYVLE 300
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|||
Db 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLRSLGLWEL 360
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QY 361 PHPWNLVVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRN-----KW 406
|||
Db 361 PHPWNLVVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKYILLFIHIYLOEPKW 420
|||

QY 407 DNRMSAMIPEDIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGIIKQYLMHYTS 466
|||
Db 421 DNRMSAMIPEDIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGIIKQYLMHYTS 480
|||

QY 467 KEDWIEHFGSKWDDFSKRKDLFDPKLLSPGQDIF 501
|||
Db 481 KEDWIEHFGSKWDDFSKRKDLFDPKLLSPGQDIF 515
|||

RESULT 6
AAG31941
ID AAG31941 standard; protein; 509 AA.
XX
AC AAG31941;
XX
DT 17-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 38445.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-00301439.
 XX
 PR 25-FEB-1999; 99US-0121825P.
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 PR 29-MAR-1999; 99US-0126785P.
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PR 30-AUG-1999; 99US-01S1303P.
PR 31-AUG-1999; 99US-01S1438P.
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PR 07-SEP-1999; 99US-01S2363P.
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PR 24-SEP-1999; 99US-01S5659P.
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PR 04-OCT-1999; 99US-01S7117P.
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PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 98.3%; Score 2551; DB 3; Length 509;
Best Local Similarity 97.2%; Pred. No. 2.1e-230;
Matches 495; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 7 MITLITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITTTVPGVICPSST 66
Db 1 MITLITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITTTVPGVICPSST 60
QY 67 ADISRLLOQAANGKSTFQVAARGQHSNLNGQASVSGGIVNMTCTIDVVVSKDKKYADVA 126
Db 61 ADISRLLOQAANGKSTFQVAARGQHSNLNGQASVSGGIVNMTCTIDVVVSKDKKYADVA 120
QY 127 AGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGQVFRNGPLVSNVLELDVIT 186
Db 121 AGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGQVFRNGPLVSNVLELDVIT 180
QY 187 KGEMELTCRQLNPFLFYGVGLGQFGIITRARIVLDPKRAKFRMLYSDFTTFTKD 246
Db 181 KGEMELTCRQLNPFLFYGVGLGQFGIITRARIVLDPKRAKFRMLYSDFTTFTKD 240
QY 247 QERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLEVAKYD 306
Db 241 QERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLEVAKYD 300

QY 307 DPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLRSLGLWELPHWLN 366
Db 301 DPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLRSLGLWELPHWLN 360
QY 367 LYVPKSRILDFHNGWVKDILLKQKSASGLALLYPTRN-----KWDNRMSA 412
Db 361 LYVPKSRILDFHNGWVKDILLKQKSASGLALLYPTRNKKYILLFIHIYLOEPKWDNRMSA 420
QY 413 MIPEIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGIIKQYLMHYTSKEDWIE 472
Db 421 MIPEIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGIIKQYLMHYTSKEDWIE 480
QY 473 HFGSKWDDFSKXKDLDFDPKLLSPGQDIF 501
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RESULT 7

AAG31942

ID AAG31942 standard; protein; 501 AA.

XX AC AAG31942;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 38446.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

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XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 30-APR-1999; 99US-0132407P.

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QY	135	LKKTAEKGVSVPVSWTDYLHITVGGTILSNGGIGQVFRNGPLVSNVLELDVITKGEMLT	C 194		
Db	121	LKKTAEKGVSVPVSWTDYLHITVGGTILSNGGIGQVFRNGPLVSNVLELDVITKGEMLT	C 180		
QY	195	SRQLNPELFYGVGLGQFGIITRARI	VLDHAPKRAKWFRLYSDFTTFTKQOERLISMA	254	
Db	181	SRQLNPELFYGVGLGQFGIITRARI	VLDHAPKRAKWFRLYSDFTTFTKQOERLISMA	240	
QY	255	NDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIIS	314		
Db	241	NDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIIS	300		
QY	315	KVIDTLTKTSLYLPFGFISMDHVA	YDFLNRVHVEENKLRSLGLWELPHPWLNLYVPKSRI	374	
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QY	375	LDFHNGVVKDILLKQKSASGLALLYPTNRN	-----KWDNRMSAMIDEIDED	420	
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KW	termination sequence.				
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Db	9	LITLITLFIISLTPTLIKSGEIDVFLPISLNLTLVTDFFSISAASHDFGNITDENPGAVL 68			
QY	62	CPSSTADISRLLOYAANG-----KSTFQVAARGQGHSLNGQASVSGGVI VNMTCI 111			
Db	69	CPSSTTEVARLLRFANGGFSYKNGSTSPASTFKVAARGQGHSLRGQASAPGGVVVNMTCI 128			
QY	112	-----TDVVVSKOKKYADVAAGTLWVDVLKKTAEKGVSPSWTDYHLHITVGGTILSNGGI 165			
Db	129	AMAAKPAAVVISADGTIADVAAGTMWVDVLKAAVDRGVSPTWTDLYLSVGGTILSNAGI 188			
QY	166	GGQVFRNGPLVSNVLELDVITKGEMLTCSRQLNPELFYVGLGGLGQFGIITRARIVLDH 225			
Db	189	GGQTRFHGPQISNVHELVDVITKGEMMTCSPKLNPELFYVGLGGLGQFGIITRARIALDH 248			
QY	226	APKRAKWFRLYSDFTTFTTKQOERLISMANDIGVDYLEGQIFLSNGVVVDTSFFPPSDQSK 285			
Db	249	APTRVKWSRIYSDFSAFKRQOERLISMTNDLGVDLEGQLMMSNGFVDTSFFPLSDQTR 308			
QY	286	VADLVKQHGIIYVLEVAKYYDDPNLPIISKVIDTLTKTSLYLPDGFISMHDVAYDFLNRV 345			
Db	309	VASLVNDHRIIYVLEVAKYYDRTTLPIDQVIDTLSRTLGFAPGFMFVQDVPYDFLNRV 368			
QY	346	HVEENKLRSLGLWELPHPWLNLYVPKSRILDFHNGVVVKDILLKQKSASGLALLYPTNRNK 405			
Db	369	RNEEDKLRSLGLWEVPHFWLNIFVPGSRIQDFHDGVINGLLNQTSTSGVTLYFPTNRNK 428			
QY	406	WDRMSAMIPEDDEDVYIIGLLQSA-TPKDLPEVESVNEKIIIRFCKDSGKIKIKOYLMHY 464			
Db	429	WNNRMSTMTP--DEDVFYVIGLLQSAGSQNWQELENLNDKVIQFCENSGIKIKIKEYLMHY 486			
QY	465	TSKEDWIEHFGSKWDDDFSKRKDLFDPKKLLSPGQDIF 501			
Db	487	TRKEDWVKHFGPKWDDFLRKIMFDPKRLSPGQDIF 523			
			RESULT 9		
			ABB93161		
ID	ABB93161 standard; protein; 524 AA.				
XX					
AC	ABB93161;				
XX					

31-MAY-2002 (first entry)
Herbicideally active polypeptide SEQ ID NO 2372.
Herbicideal; plant; agriculture; herbicide.
Arabidopsis thaliana.

WO200210210-A2.

07-FEB-2002.

28-AUG-2001; 2001WO-EP009892.

28-AUG-2001; 2001WO-EP009892.

(FARB) BAYER AG.

Tietjen K, Weidler M;

WPI; 2002-269010/31.

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.

Claim 5; SEQ ID NO 2372; 261pp + Sequence Listing; English.

The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides

Sequence 524 AA;

Query Match 70.2%; Score 1822; DB 5; Length 524;
Best Local Similarity 66.7%; Pred. No. 7.2e-162;
Matches 345; Conservative 69; Mismatches 79; Indels 24; Gaps 5;

QY 7 MITLITVLM-----ITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTTPGGVI 61
Db 9 LITLITLIFISLTPTLIKSDGIDVFLPISLNLTLVLTDPFISISAASHDFGNITDENPGAVL 68
QY 62 CPSSSTADISRLLOAANG-----KSTFQVAARGQGHSLNGQASVSGGVIVNMTCI 111
Db 69 CPSSSTEVARLLRFANGFYSYKNGSTSPASTFKVAARGQGHSLRGQASAPGVVNMTC 128
QY 112 -----TDVWVSKDKKYADVAAAGTLWVDVLKKTAEKGVSPVSWTDYHLHITVGGTSLNNGGI 165
Db 129 AMAAKPAAVVISADGTYADVAAAGTMWVDVLKAAVDRGVSPVTWTDYLSVGGTSLNAGI 188
QY 166 GGQVFRNGPLVSNVLELDVITKGEMLTCSRQLNPFLFYGVGLGQFGIITRARIVL 225
Db 189 GGQTFRHGPQISNVHELVDVITCKGEMMTCSPKLNPELPHYGVGLGQFGIITRARI 248
QY 226 APKRAKWRMLYSDFTTFTTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSK 285
Db 249 APTRVWKSRLYSDFSFAFKRDQERLISMTNDLGVDFLEGQLMNSNGFVDTSFPLSDQTR 308
QY 286 VADLVQKHGIIYVLEVAKYDDPNLPIISKVIDTLTKLSYLPFGFISMHDVAFDFLNRV 345
Db 309 VASLVNDHRIIYVLEVAKYIDRTPLPIDQVIDTLSTRILGFAPGFMFVQDVPYDFLNRV 368
QY 346 HVEENKLSLGLWELPHPLNLVYPKSRILDFHNGVVKDILLKQKSASGLALLPTNRNK 405
Db 369 RNEEDKLSLGLWEVPHPLNLFVPGSRIQDFHDGVINGLLNQTSTSGVTLLFPTNRNK 428

QY 406 WDNRMSAMIPEDIEDVIYIIGLQSA-TPKDLPEVESVNEKIIRFCDSGIIKQYLMHY 464
Db 429 WNNRMSTWTP--DEDVFYVIGLQAGGSQNWQLENLNDKVIOFCENSIGIKIKEYLMHY 486
QY 465 TSKEDWIEHFGSKWDDFSCRKDLFDPKKLLSPGQDIF 501
Db 487 TRKEDWVKHFGPKWDDFLRKKIMFDPKRLSPGQDIF 523

RESULT 10

AAU81970

ID AAU81970 standard; protein; 524 AA.

XX AAU81970;

DT 09-APR-2002 (first entry)

DE A. thaliana cytokinin oxidase AtCKX4.

KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;
KW root growth; lateral root; adventitious root; root geotropism; herbicide;
KW root meristem; shoot meristem; leaf senescence; parthenocarp.

XX Arabidopsis thaliana.

XX WO200196580-A2.

XX 20-DEC-2001.

XX 18-JUN-2001; 2001WO-EP006833.

XX 16-JUN-2000; 2000EP-00870132.

XX 27-DEC-2000; 2000US-0258415P.

XX 16-MAR-2001; 2001EP-00870053.

XX (SCHM/) SCHMULLING T.

XX (WERN/) WERNER T.

XX Schmulling T, Werner T;

XX WPI; 2002-130736/17.

XX N-PSDB; ABK28609.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase activity and the protein useful for stimulating root growth, enhancing the formation of lateral or adventitious roots, altering root geotropism.

XX Claim 2; Page 135-137; 154pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding a novel plant protein (II) having cytokinin oxidase activity. (I) is useful for production of transgenic plants, plant cells or tissues; for production of altered plants, plant cell or tissues; and for effecting the expression of (II) where (I) is operably linked to one or more control sequences. The methods further comprises regenerating a plant from the plant cell. (I) and (II) are useful for stimulating root growth; enhancing the formation of lateral or adventitious roots; altering root geotropism, leading to an increase in yield; and for screening growth promoting chemical of herbicides. (I) is useful for increasing the size of the root meristem; increasing root size; increasing the size of the shoot meristem; delaying leaf senescence and altering leaf senescence; increasing leaf thickness; reducing or increasing the vessel size; inducing parthenocarp; improving standability of the seedlings; increasing branching and for improving lodging resistance. Antibody (III) to (II) is useful for identifying and obtaining proteins interacting with (II) comprising a screening assay, preferably a two-hybrid screening assay. AAU81967-AAU81974 represent Arabidopsis thaliana cytokinin oxidase amino acid sequences

XX Sequence 524 AA;

Query Match 70.2%; Score 1822; DB 5; Length 524;
Best Local Similarity 66.7%; Pred. No. 7.2e-162;

QY	162	NGGIGQVFRNGPLVSNVLELDVITGKGMITCSRQNPFLFYGLGGLGQFGIITRARI	221
Db	61	NAGIGGQTFRHGPQISNVHELVDVITGKGMWTCSPKLNPELFYGLGGLGQFGIITRARI	120
QY	222	VLDHAPKRAKWFRLYSDFTTFTKQOERLISMANDIGVDYLEGOIFLSNGVWDTSEFFPPS	281
Db	121	ALDHAPTRVKWSRILYSDFAFKRDQOERLISMTNDLGVDLFLEGQLMMSNGFVDTSEFFPLS	180
QY	282	DQSKVADLVKQHGIIVLEVAKYYDDPNLPISKVIDTLTKTLSYLPGFISMHDVAYEDF	341
Db	181	DQTRVASLVNDHRIIVLEVAKYYDRTTLPIIDQVIDTLTSLTGFAPGFMEVQDVPYFDF	240
QY	342	LNRVHVEENKRLSLGLWELPHPWLNLYVPKSRILDPHNGVVKDILLKQKSASGLALLYPT	401
Db	241	LNRVRNEEDKRLSLGLWEVPHPWLNIFVPGSRIQDFHGDGVINGLLNQTSTSGVTIFYPT	300
QY	402	NRNKWNRMSAMIPEDVDVYIIGLLQSA-TPKDLPEVESVNEKIIRFCKDSGIIKIQY	460
Db	301	NRNKWNRMSTMT-DEDVFYVIGLLQSAAGGSQNWQELENLNDKVIOFCENSIIKIREY	358
QY	461	LMHYTSKEDWIEHFGSKWDDFSKRKOLFDPKLLSPGQDIF	501
Db	359	LMHYTRKEDWVKHFGPKWDDFLRKIMFDPKRLSPGQDIF	399
RESULT 14			
AAG31318			
ID	AAG31318 standard; protein; 395 AA.		
XX			
AC	AAG31318;		
XX			
DT	17-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 37591.		
XX			
KW	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-00301439.		
XX			
PR	25-FEB-1999;	99US-0121825P.	
PR	05-MAR-1999;	99US-0123180P.	
PR	09-MAR-1999;	99US-0123548P.	
PR	23-MAR-1999;	99US-0125788P.	
PR	25-MAR-1999;	99US-0126264P.	
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PR	01-JUN-1999;	99US-0137222P.	
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PR	25-OCT-1999;	99US-0145913P.
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PR	29-OCT-1999;	99US-0162142P.
Query Match 58.0%; Score 1505.5; DB 3; Length 395;		
Best Local Similarity 71.0%; Pred. No. 2.6e-132;		
Matches 276; Conservative 54; Mismatches 56; Indels 3; Gaps 2;		
QY	114	VVYSKDKKYADVAAGTILWVDVLKKTAEKGVSPVSWTDYLHITVGGTILNGIGGQVFRNG 173
Db	8	VVISADGTYADVAAGTWWVDVLKAAVDRGVSPVTWTDYLYLSVGGTILSNAGIGGQTFRHG 67
QY	174	PLVSNVLELDVITGKGEMLTCSRQLNPFLFYGLGGLGQFGIITRARIVLHDHAPKRAKWF 233
Db	68	PQISNVHELDVITGKGEMTCSPKLNPELFYGLGGLGQFGIITRARIALDHAPTRVKS 127
QY	234	RMLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQH 293
Db	128	RILYSDFSAFKRDQERLISMTNDLGVDLEGQLMMSNGFVDTTSFFPLSDQTRVASLVNDH 187
QY	294	GIYVLEVAKYYDDPNLPIISKVIDTLTKTLSYLPGFISMHDVAYFDFLNRVHVEENKLR 353
Db	188	RIYVLEVAKYYDRRTLPIIDQVIDTLSTRTGFAFGFMFQDVPYFDFLNRVNEEDKLR 247
QY	354	SLGLWELPHPWLNLVVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWNRMSAM 413
Db	248	SLGLWEVPHPWLNIFVPGSRIQDFHDGVINGLLNLTSTSGVTLFYPTNRNKNWNRMSTM 307
QY	414	IPEIDEDVIYIIGLLQSA-TPKDLPEVESVNEKIIREFCKDSGIIKIKQYLMHYTSKEDWIE 472
Db	308	TP--DEDVYFVIGLLQSAGSQNWQELENLNDKVIQFCENSGIKIKEYLHYTRKEDWVK 365
QY	473	HFGSKWDDFSCRKDLFDPKLLSPGQDIF 501
Db	366	HFGPKWDDFLRKKIMFDPKRLSPGQDIF 394
RESULT 15		
ID	ABB93847	standard; protein; 523 AA.
XX	ABB93847;	
AC	ABB93847;	
XX	31-MAY-2002	(first entry)
DT	31-MAY-2002	(first entry)
XX	Herbicide	Herbicide
DE	Herbicide	Herbicide
XX	Herbicide	Herbicide
KW	Herbicide	Herbicide
XX	Herbicide	Herbicide
OS	Arabidopsis thaliana.	
XX	WO200210210-A2.	
PN	WO200210210-A2.	
XX	07-FEB-2002.	
PD	07-FEB-2002.	
XX	28-AUG-2001;	2001WO-EP009892.
PF	28-AUG-2001;	2001WO-EP009892.
XX	28-AUG-2001;	2001WO-EP009892.
PR	(FARB)	BAYER AG.
XX	Tietjen K,	Weidler M;
PI	Tietjen K,	Weidler M;
XX	WPI;	2002-269010/31.
DR	WPI;	2002-269010/31.
XX	Identifying plant target	proteins for herbicidally active compounds,
PT	comprising aligning and comparing	nucleic acid or amino acid sequences

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 17:42:01 ; Search time 21 Seconds
(without alignments)
2294.855 Million cell updates/sec

Title: US-10-014-101-4

Perfect score: 2596

Sequence: 1 MANLRMLTITVLMITKSS.....SKRKDLFPDKLLSPGQDIF 501

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2579	99.3	515	2 E84577	probable cytoxinin
2	1822	70.2	524	2 T09937	cytoxinin oxidase
3	1152	44.4	534	2 T51929	cytoxinin oxidase
4	1141	44.0	534	2 T01500	cytoxinin oxidase
5	1079	41.6	512	2 B96785	hypothetical prote
6	1056.5	40.7	575	2 T00807	probable cytoxinin
7	993	38.3	504	2 T49185	cytoxinin oxidase
8	567.5	21.9	438	2 E55578	hypothetical prote
9	429	16.5	447	2 AC1847	hypothetical prote
10	196.5	7.6	470	2 H70795	hypothetical prote
11	196	7.6	479	2 B95997	probable oxidoredu
12	195	7.5	511	2 T48777	6-HYDROXY-D-NICOTI
13	190	7.3	466	2 T49756	related to berberi
14	183.5	7.1	459	2 A87201	conserved hypothet
15	177.5	6.8	610	2 T06690	Galactonolactone d
16	177	6.8	445	2 T35893	FAD-dependent oxid
17	177	6.8	461	2 H69350	glycolate oxidase
18	175.5	6.8	600	2 T14463	Galactonolactone d
19	175	6.7	460	2 E86922	probable FAD-link
20	173.5	6.7	466	2 B69842	probable oxidoredu
21	172.5	6.6	461	2 B70697	probable oxidoredu
22	168.5	6.5	539	2 T10626	reticuline oxidase
23	168	6.5	440	1 OXRTGU	L-gulonolactone ox
24	167.5	6.5	461	2 A70687	probable oxidoredu
25	164	6.3	470	2 D69984	glycolate oxidase
26	161.5	6.2	540	2 T10625	reticuline oxidase
27	161	6.2	447	2 G70034	reticuline oxidase
28	159	6.1	535	2 T07969	probable reticul
29	154.5	6.0	482	2 C70452	D-lactate dehydrog

mcrA protein - Str
FAD/FMN-containing
hypothetical prote
probable oxidoredu
hypothetical prote
D-lactate dehydrog
hypothetical prote
D-lactate dehydrog
reticuline oxidase
probable sorbitol
probable oxidase
probable oxidase y
conserved hypothet
hypothetical prote
probable iron-sulf
probable oxidoredu

ALIGNMENTS

RESULT 1

E84577

probable cytoxinin oxidase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 19-Apr-2002

C:Accession: E84577

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: E84577

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-515 <STO>

A:Cross-references: GB:AE002093; NID:g4191780; PIDN:AAD10149.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g19500

A:Map position: 2

C:Superfamily: poppy reticuline oxidase

Query Match 99.3%; Score 2579; DB 2; Length 515;
Best Local Similarity 97.3%; Pred. No. 2e-172;
Matches 501; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSLTDPSIIISAASHDFGNITVTPGGV 60

Db 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSLTDPSIIISAASHDFGNITVTPGGV 60

QY 61 ICPSSTADISRLQLQYAANGKSTFQVAARGQGHSLNGQASVSGGVINMTCTIDVVVSKDK 120

Db 61 ICPSSTADISRLQLQYAANGKSTFQVAARGQGHSLNGQASVSGGVINMTCTIDVVVSKDK 120

QY 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYHLITVGGTSLNGGIGGQVFRNGPLVSNVL 180

Db 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYHLITVGGTSLNGGIGGQVFRNGPLVSNVL 180

QY 181 ELDVITKGEMLTCSRQLNPELFYGVGLGQFGIITRARIVLDPAPKRAKWFRLYSDF 240

Db 181 ELDVITKGEMLTCSRQLNPELFYGVGLGQFGIITRARIVLDPAPKRAKWFRLYSDF 240

QY 241 TTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSPDSQKVADLVKQHGIIYVLE 300

Db 241 TTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSPDSQKVADLVKQHGIIYVLE 300

QY 301 VAKYYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLSRLGLWEL 360

Db 301 VAKYYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLSRLGLWEL 360

QY 361 PHPWNLNLYVPKSRILDFPHNGVVKDILLKQKSASGLALLYPNTNRN-----KW 406

|||||

Db 361 PHPWNLVVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKYILLFIHIYLOEPKW 420
Qy 407 DNRMSAMIPEDIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGKIKQYLMHYTS 466
Db 421 DNRMSAMIPEDIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRFCKDSGKIKQYLMHYTS 480
Qy 467 KEDWIEHFGSKWDDFSKXKDLDFDPKLLSPGQDIF 501
Db 481 KEDWIEHFGSKWDDFSKXKDLDFDPKLLSPGQDIF 515

RESULT 2
T09937
cytokinin oxidase homolog T16L4.250 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jun-2002
C;Accession: T09937
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16897
A;Accession: T09937
A;Molecule type: DNA
A;Residues: 1-524 <BEV>
A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.250
A;Experimental source: cultivar Columbia; BAC clone T16L4
C;Genetics:
A;Gene: ATSP:T16L4.250
A;Map position: 4
A;Introns: 210/1; 252/3; 338/3; 428/2

Query Match 70.2%; Score 1822; DB 2; Length 524;
Best Local Similarity 66.7%; Pred. No. 1.7e-119;
Matches 345; Conservative 69; Mismatches 79; Indels 24; Gaps 5;

Qy 7 MITLITVLM-----ITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTTPGGVI 61
Db 9 LITLITLIFSLTPTLIKSDGIDVFLPISLNLTLVTDPPSISAASHDFGNITDENPGAVL 68

Qy 62 CPSSSTADISRLLQYAANG-----KSTFQVAARGQHSNLNGQASVSGGVVNMTCI 111
Db 69 CPSSSTEVARLLRFANGGFSYNGKSTSPASTFKVAARGQHSNLRGQASAPGGVVNMTCI 128

Qy 112 -----TDVVVSKKKYADVAAGTILWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGI 165
Db 129 AMAAKPAVVISADGTYADVAAGTIVVDVLKAAVDRGVSPVTWTDYLYLSVGGTSLNAGI 188

Qy 166 GGQVFRNGPLVSNVLELDVITKGEMLTCSRQLNPPELFYVGLGGLGQFGIITRARIIVLDH 225
Db 189 GGQTFRHGPQISNVHELVDVITKGEMTCSPKLNPPELFYVGLGGLGQFGIITRARIIVLDH 248

Qy 226 APKRAKWRMLYSDFTTFTTKDQERLISMANDIGVDYLEGQIFLSNGVWDTSTFFPDSQSK 285
Db 249 APTRVKWSRILYSDFSFAFKRDQERLISMTNDLGVDFLEGQLMMSGFVDTSTFFPLSDQTR 308

Qy 286 VADLVKQHGLIYVLEVAKYYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRV 345
Db 309 VASLVNDRHRIYVLEVAKYYDRITLPIIDQVIDTLSTRTLGFAPGMFVQDVPYFDFLNRV 368

Qy 346 HVEENKLSLGLWELPHWPNLNLVYVPSRILDFHNGVVKDILLKQKSASGLALLYPTNRNK 405
Db 369 RNEEDKLSLGLWEVPHWPNLNLVYVPSRIQDFHDGVINGLLLNQTSSTSGVTLFYPTNRNK 428

Qy 406 WDNRMMSAMTPEIDEDVIYIIGLLQSA-TPKDLPEVESVNEKIIRFCKDSGKIKQYLMHY 464
Db 429 WNNRMSTWTP--DEDVFYVIGLLQSAAGSQNWQELNLDKVIQFCENSGIKIKEYLMHY 486

Qy 465 TSKEDWIEHFGSKWDDFSKXKDLDFDPKLLSPGQDIF 501
Db 487 TRKEDWVXHFPGKWDDFLRKKIMFDPKRLSPGQDIF 523

RESULT 3
T51929

cytokinin oxidase [imported] - maize
C;Species: Zea mays (maize)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T51929
R;Houba-Herlin, N.; Pethe, C.; D'Alayer, J.; Laloue, M.
Plant J. 17, 615-626, 1999
A;Title: Cytokinin oxidase from Zea mays : purification, cDNA cloning and expression in
A;Reference number: Z25869
A;Accession: T51929
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-534 <HOU>
A;Cross-references: EMBL:Y18377; PIDN:CAA77151.1
A;Experimental source: cultivar nobilis
C;Genetics:
A;Gene: cko

Query Match 44.4%; Score 1152; DB 2; Length 534;
Best Local Similarity 47.4%; Pred. No. 1.1e-72;
Matches 235; Conservative 84; Mismatches 149; Indels 28; Gaps 11;

Qy 30 SLNLTSTDPSSIISAASHDFGNITVTTPGGVICPSSTADISRLLQYAANGKS--TFQVAA 87
Db 42 ALDGKLRDTSNATAAASDFTGNITSALPAAVLYPSSTADLVALLS-AANSTFGWPYTIAP 100

Qy 88 RGQHSNLNGQASVSGGVVNMTCITD-----VVVSKKKYADVAAGTILWVDVLKKTAEK 141
Db 101 RGRGHSNLNGQAFAPGGVVVNMASLGDAAAAPRINVSADGRYVDAGGEQVWIDVLRASLAR 160

Qy 142 GVSPVSWTDYLHITVGGTSLNGGIGGQVFRNGPLVSNVLELDVITKGEMLTCSRQLNPE 201
Db 161 GVAPRSWTDYLYLTVGGTSLNAGISGQAFRHGPQISNVLEMDVITGHGEMVTCSKQLNAD 220

Qy 202 LFYGVGLGGLGQFGIITRARIIVLDHAPKRAKWRMLYSDFTTFTTKDQERLISMANDIG-- 258
Db 221 LFDAVLGGLGQFGVITRARIIVAEVPAPARARWVRLVYTDFAAFSADQERLTAPRPGGGAS 280

Qy 259 ---VDYLEGQIF---LSNGVVDTSFFPPSDQSKVADLVKQHG--IYVLEVAKYYDDPN 309
Db 281 FGPMYSVEGSVFVNQSLATDLANTGFFTDADVARIVALAGERNATTVYSIEATLNYDNAT 340

Qy 310 --LPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLSLGLWELPHWPNL 367
Db 341 AAAAAVDQELASVLGTLVYVEGFQFQDVAAYAAFLDRVHGEVALNKLGLWRVPHWPNLN 400

Qy 368 YVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKWNRMSAMIPEIDEDVIYIIGL 427
Db 401 FVPRSRITADFRGVFKGI-LQGTDIVGPLIVYPLNKSMMWDDGMSAATP--SEDFVFAVSL 457

Qy 428 L-QSATPKDLPEVESVNEKIIRFCKDSGKIKQYLMHYTSKEDWIEHFG-SKWDDFSXKK 485
Db 458 LFSSVAPNDLARLQEQNRRLRFLCDLAGIQKTYLARHTDRSDVVRHFGAAKWRNFVEMK 517

Qy 486 DLFDPPKLLSPGQDIF 501
Db 518 NKYDPKRLSPGQDIF 533

RESULT 4
T01500

cytokinin oxidase 1 - maize
C;Species: Zea mays (maize)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Oct-1999
C;Accession: T01500
R;Morris, R.O.; Laskey, J.G.
submitted to the EMBL Data Library, January 1998
A;Description: A glycosylated cytokinin oxidase from maize.
A;Reference number: Z14336
A;Accession: T01500
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-534 <MOR>
A;Cross-references: EMBL:AF044603; NID:G3341977; PIDN:AA27500.1; PID:G3341978

QY **Dd**

394 GLALLYPTNRNKNWDRMSAMTPEIDEDVYYIIGLLQSATPKDLPEVESVNEKIIRFCXDS 453
|| : || | : || | : || : || : || : || :

332 GLIMVYPITPP---ITAPFIPIPHCDTFMFLAVLRTASPGAEARMIASNRLLLYEQARDV 388
| : || | : || | : || : || : || : || :

QY

454 GIKIQYLHMYTSKEDIWHFGSKWDDEFKRKDLDPKKLSPG 497
| || | || | || | || : || : || : || :

Dd

389 GGVAAYAVNAVPMSPGDWCCTHFGRWQAIAARAKRRFDPYRILAPG 432

RESULT 9

ACl847

hypothetical protein all0324 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: ACl847

R.;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana-

A;Reference number: AB1807; UID:21595285; PMID:11759840

A;Accession: ACl847

A>Status: preliminary

A:Molecule type: DNA

A;Residues: 1-447 <CUR>

A;Cross-references: GB:BA000019; PIDN:BAB72282.1; PID:g17129669; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alio324

H70795
hypothetical protein Rv3719 - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C/Accession: H70795
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: H70795
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-470 <COL>
A/Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18041.1; PID:el264579
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: Rv3719

OM protein - protein search, using sw model

Run on: April 5, 2004, 17:38:21 ; Search time 17 Seconds
(without alignments)
1534.538 Million cell updates/sec

Title: US-10-014-101-4
Perfect score: 2596
Sequence: 1 MANRLMITLITVLMITKSS.....SKRKOLFDPKLLSPGQDIF 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2596	100.0	501	1	CKX2_ARATH	Q9fuj3 arabidopsis
2	1822	70.2	524	1	CKX4_ARATH	Q9fuj2 arabidopsis
3	1292	49.8	523	1	CKX3_ARATH	Q9lts3 arabidopsis
4	1152	44.4	534	1	CKX1_MAIZE	Q9t0n8 zea mays (m
5	1143	44.0	532	1	CKX1_ORYSA	Q9lde6 oryza sativ
6	567.5	21.9	438	1	FAS5_RHOFA	P46377 rhodococcus
7	214.5	8.3	458	1	HDNO_ARTOX	P08159 arthrobacte
8	169	6.5	439	1	GGLO_RAT	P10867 rattus norv
9	159	6.1	535	1	RETO_PAPSO	P93479 papaver som
10	153.5	5.9	447	1	MCRA_STRLA	P43485 streptomyc
11	153	5.9	439	1	GGLO_MOUSE	P58710 mus musculu
12	149	5.7	538	1	RETO_ESCCA	P30986 eschschoelzi
13	148	5.7	418	1	XVOA_STRCO	Q9zbul streptomyc
14	147	5.7	1018	1	YDIJ_ECOLI	P77748 escherichia
15	144.5	5.6	496	1	DLD3_YEAST	P39976 saccharomyc
16	140	5.4	440	1	GGLO_SCYTO	Q90yk3 scyliorhinu
17	139.5	5.4	587	1	DLD1_YEAST	P32891 saccharomyc
18	135.5	5.2	1027	1	YDIJ_HAEIN	Q57252 haemophilus
19	133	5.1	723	1	Y262_HAEIN	P44600 haemophilus
20	131	5.0	557	1	ALO_CANAL	Q93852 candida alb
21	130.5	5.0	579	1	DLD1_KLULA	Q12627 kluyveromyc
22	130	5.0	613	1	ADAS_TRYBB	O97157 trypanosoma
23	129.5	5.0	526	1	ALO_YEAST	P54783 saccharomyc
24	126.5	4.9	415	1	XVOA_STRSQ	Q9kx73 streptomyc
25	124	4.8	611	1	ADAS_DICDI	O96759 dictyosteli
26	123	4.7	499	1	GLCD_ECOLI	P52075 escherichia
27	122.5	4.7	530	1	AIP2_YEAST	P46681 saccharomyc
28	118	4.5	484	1	YGCU_ECO57	Q8x780 escherichia
29	117	4.5	516	1	DHCR_HUMAN	Q15392 homo sapien
30	116	4.5	725	1	HXC2_HAEIN	P45357 haemophilus
31	112	4.3	484	1	YGCU_ECOLI	Q46911 escherichia
32	111	4.3	658	1	ADAS_CAVPO	P97275 cavia porce
33	110	4.2	1012	1	POLS_IBDVA	P08364 avian infec

34	108	4.2	344	1	SYW_CHLPN	Q9z7a4 chlamydia p
35	108	4.2	512	1	VC02_VACCV	P17371 vaccinia vi
36	108	4.2	561	1	DIM_ARATH	Q39085 arabidopsis
37	108	4.2	658	1	ADAS_HUMAN	Q00116 homo sapien
38	107.5	4.1	793	1	SYFB_CLOPE	Q8xj76 clostridium
39	107	4.1	662	1	POFA_SCHPO	Q9p7w4 schizosacch
40	106.5	4.1	512	1	VC02_VACCC	P21037 vaccinia vi
41	106	4.1	1290	1	VACA_HELPY	P55981 helicobacte
42	106	4.1	1953	1	BIGA_SALTY	P25927 salmonella
43	105	4.0	513	1	CP12_MOUSE	P00186 mus musculu
44	105	4.0	1012	1	POLS_IBDVC	P15480 avian infec
45	104	4.0	1012	1	POLS_IBDVS	P25219 avian infec

ALIGNMENTS

RESULT 1

ID	CKX2_ARATH	STANDARD;	PRT;	501 AA.
AC	Q9FUJ3; Q9ZUP1;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Cytokinin oxidase 2 precursor (EC 1.4.3.-) (CKO 2).			
GN	CKX2 OR AT2G19500 OR F3P11.10.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21068113; PubMed=11154345;			
RA	Bilyeu K.D., Cole J.L., Laskey J.G., Riekhof W.R., Esparza T.J.,			
RA	Kramer M.D., Morris R.O.;			
RT	"Molecular and biochemical characterization of a cytokinin oxidase			
RT	from maize.";			
RL	Plant Physiol. 125:378-386(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=20083487; PubMed=10617197;			
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,			
RA	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,			
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,			
RA	Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,			
RA	Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,			
RA	Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,			
RA	Salzberg S.L., Fraser C.M., Venter J.C.;			
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis			
RT	thaliana.";			
RL	Nature 402:761-768(1999).			
CC	-!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of			
CC	N(6)-substituted adenine derivatives that are plant hormones,			
CC	where the substituent is an isopentenyl group.			
CC	-!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +			
CC	O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).			
CC	-!- COFACTOR: FAD (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Extracellular.			
CC	-!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked			
CC	oxidoreductase family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF303978; AAC30905.1; -.			
DR	EMBL; AC005917; AAD10149.2; -.			

DR InterPro; IPR006094; Oxid_FAD bind.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR InterPro; IPR009014; Transketo_C_like.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; 1.
KW Oxidoreductase; Flavoprotein; FAD; Multigene family; Signal;
KW Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 501 CYTOKININ OXIDASE 2.
FT BINDING 92 92 FAD (COVALENT) (BY SIMILARITY).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 157 157 G -> R (IN REF. 1).
SQ SEQUENCE 501 AA; 55583 MW; 9F8F0AAEAA4DE84A CRC64;
Query Match 100.0%; Score 2596; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 4.7e-170;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANRLMITLITVLMITKSNIGKIDLPKSLNLTSTDPSSIISAASHDFGNITVTGGV 60
Db 1 MANRLMITLITVLMITKSNIGKIDLPKSLNLTSTDPSSIISAASHDFGNITVTGGV 60
QY 61 ICPSTADISRLQLYAANGKSTFQVAARGQGHSLNGQASVSGVIVNMTCTDVVWSKDK 120
Db 61 ICPSTADISRLQLYAANGKSTFQVAARGQGHSLNGQASVSGVIVNMTCTDVVWSKDK 120
QY 121 KYADVAAGTLWVDLVKLTAKGVSPVSWTDYLTHTVGGTSLNGIGGVFRNGPLVSNVL 180
Db 121 KYADVAAGTLWVDLVKLTAKGVSPVSWTDYLTHTVGGTSLNGIGGVFRNGPLVSNVL 180
QY 181 ELDVITGKGEMLTCSRQLNPFLFYGLVGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
Db 181 ELDVITGKGEMLTCSRQLNPFLFYGLVGLGQFGIITRARIIVLDHAPKRAKWFRLYSDF 240
QY 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
Db 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
QY 301 VAKYDDPNLPIISKVIDTLTKTSLYLPFGFISMDVAYFDFLNRVHVEENKLSLGLWEL 360
Db 301 VAKYDDPNLPIISKVIDTLTKTSLYLPFGFISMDVAYFDFLNRVHVEENKLSLGLWEL 360
QY 361 PHPWNLVYVPSKRIILDFHNGVVKDILLKQKASGLALLYPTNRNKNWNRMSAMPEIDED 420
Db 361 PHPWNLVYVPSKRIILDFHNGVVKDILLKQKASGLALLYPTNRNKNWNRMSAMPEIDED 420
QY 421 VIYIIGLLQSATPKDLPEVESVNEKIIRFCCKDSGKIKIKQYLMHYTSKEDWIEHFGSKWDD 480
Db 421 VIYIIGLLQSATPKDLPEVESVNEKIIRFCCKDSGKIKIKQYLMHYTSKEDWIEHFGSKWDD 480
QY 481 FSKRKDLDFDPKLLSPGQDIF 501
Db 481 FSKRKDLDFDPKLLSPGQDIF 501

RESULT 2
CKX4 ARATH STANDARD; PRT; 524 AA.
AC Q9FUJ2; Q9SU77;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cytokinin oxidase 4 precursor (EC 1.4.3.-) (CKO 4).
GN CKX4 OR AT4G29740 OR T16L4.250.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21068113; PubMed=11154345;
RA Bilyeu K.D., Cole J.L., Laskey J.G., Riekhof W.R., Esparza T.J.,
RA Kramer M.D., Morris R.O.;
RT "Molecular and biochemical characterization of a cytokinin oxidase
from maize."
RL Plant Physiol. 125:378-386 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutery M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysschaert C., Gielens J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.-A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Gaisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosomes 4 of the plant Arabidopsis
thaliana."
RL Nature 402:769-777 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis

KW Glycoprotein. 1 31 POTENTIAL.
 FT SIGNAL 32 523 CYTOKININ OXIDASE 3.
 FT CHAIN 105 105 FAD (COVALENT) (BY SIMILARITY).
 FT BINDING 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 523 AA; 59422 MW; 2324EFPC21D7103A CRC64;

Query Match 49.8%; Score 1292; DB 1; Length 523;
 Best Local Similarity 48.5%; Pred. No. 6.8e-81;
 Matches 251; Conservative 106; Mismatches 138; Indels 22; Gaps 6;

QY 3 NLRMLITLIT---VLMITKSSNGIKIDLPKSLNL-----TLSTDPSIISAASHDFGN 51
 DB 5 NLRQVRLIAITVITLSTPITTTNPQPWNILSHNEFACKLTSSSSSVESATDFGH 64
 QY 52 ITTTPGGVICPSTADISRLQLQYAANGKSTFQVAARGQGHSLNGQASVSGGVVNMTCI 111
 DB 65 VTKIFPSAVLIPSSVEDITDLKLSFDSQLSFPLAARGHSHRGQASAKDGVVNMVMSR 124
 QY 112 TD---VVVSKDKKYADVAAGTLWVDVLKKTAEKGVSPVSTDYHLITVGGTILSGGIGG 167
 DB 125 VNRDRGKIVSRCLYVDVDAWLWIEVINKTLEGLTPVSTDYLYLTVGGTILSGGIGS 184
 QY 168 QVFRNGPLVSNVLELDVITKGEMLTCSRQLNPPELFGVGLGQFGIITRARIVDHAP 227
 DB 185 QTFRYGPOITVLEMDVITKGGEIATCSKDMNSDLFFAVLGLGQFGIITRARIKLEVP 244
 QY 228 KRAKWRMLYSDFTFETKQERLISMANDIGVDYLEGQIFLSNGVVD---TSFPPPSDQS 284
 DB 245 KRAKWLRLFLYIDFSEFTRDQERVISKTD--GVDFLEGSIMVDHGPPDNWRSTYPPSDHL 302
 QY 285 KVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKLTLVLPFGFISMHDVAYDFLNR 344
 DB 303 RIASMKRHRVYCLEVVKYDETSQYTVNEEMEELSDSLNHRVGFMYEKDVTYMDFLNR 362
 QY 345 VHVEENKRLSLGLWELPHPLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRN 404
 DB 363 VRTGELNLKSKGQWDVPHPLNLFVPTKQISKFDGDFVFGKILRNITSGPVLVPMVNRN 422
 QY 405 KWDNRMSAMIPEDDEDVYIIGLQSATPKDLPEVESVNEKIIRFCKDSGIKIKOYLMHY 464
 DB 423 KWNDRMSAAIPE--EDVFYAVGFLRSAGFDNWEAFDQENMEILKFCEDANMGVIQYLPYH 480
 QY 465 TSKEDWIEHFGSKWDDFSKRKDLDFDKKLLSPGQDIF 501
 DB 481 SSQEGVVRHFGPRWNIFVERKYKYDPPKMLSPGQNI 517

RESULT 4

CKX1_MAIZE STANDARD; PRT; 534 AA.
 AC Q9TON8; O81158;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cytokinin oxidase 1 precursor (EC 1.4.3.-) (CKO 1).
 GN CKX1.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 417-435; 490-517 AND 524-534.
 RC STRAIN=cv. Nobilis; TISSUE=kernel;
 RX MEDLINE=99246676; PubMed=10230061;
 RA Houba-Herlin N., Pethe C., D'Alayer J., Laloue M.;
 RT "Cytokinin oxidase from Zea mays: purification, cDNA cloning and
 expression in moss protoplasts.";
 RL Plant J. 17:615-626(1999).
 RN [2]
 RP SEQUENCE FROM N.A., SEQUENCE OF 286-308; 369-377; 388-392 AND 417-431,

RP AND MASS SPECTROMETRY.
 RX MEDLINE=99160863; PubMed=10049708;
 RA Morris R.O., Bilyeu K.D., Laskey J.G., Cheikh N.N.;
 RT "Isolation of a gene encoding a glycosylated cytokinin oxidase from
 maize.";
 RL Biochem. Biophys. Res. Commun. 255:328-333(1999).
 RN [3]
 RP CHARACTERIZATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=21068113; PubMed=1154345;
 RA Bilyeu K.D., Cole J.L., Laskey J.G., Riekhof W.R., Esparza T.J.,
 RA Kramer M.D., Morris R.O.;
 RT "Molecular and biochemical characterization of a cytokinin oxidase
 from maize.";
 RL Plant Physiol. 125:378-386(2001).
 CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
 substituted adenine derivatives that are plant hormones, where the
 substituent is an isopentenyl group. Cleaves zeatin,
 isopentenyladenine, isopentenyladenosine, zeatin riboside and cis-
 zeatin, but not dihydrozeatin, kinetin and benzylaminopurine.
 CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +
 O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).
 CC -!- COFACTOR: FAD.
 CC -!- ENZYME REGULATION: Competitive inhibition by phenylureas.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: Expressed in immature kernels and unpollinated
 cobs. Weakly expressed in kernels harvested two weeks after
 anthesis.
 CC -!- PTM: Glycosylated, with approximately 10 hexose residues per site.
 CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
 oxidoreductase family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Y18377; CAA77151.1; --
 CC EMBL; AF044603; AAC27500.1; --
 CC PIR; T01500; T01500.
 CC PIR; T51929; T51929.
 CC MaizeDB; 194080; --
 CC InterPro; IPR006094; Oxid_FAD bind.
 CC InterPro; IPR006093; Oxid_FAD_BS.
 CC Pfam; PF01565; FAD binding 4; 1.
 CC PROSITE; PS00862; OX2_COVAL_FAD; 1.
 KW Oxidoreductase; Flavoprotein; FAD; Signal; Glycoprotein.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 534 CYTOKININ OXIDASE 1.
 FT DOMAIN 339 345 POLY-ALA.
 FT BINDING 105 105 FAD (COVALENT) (PROBABLE).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 79 79 A -> G (IN REF. 2).
 FT CONFLICT 168 168 T -> N (IN REF. 2).
 FT CONFLICT 254 254 L -> F (IN REF. 2).
 SQ SEQUENCE 534 AA; 57195 MW; 3DE671BC4F40918B CRC64;

Query Match 44.4%; Score 1152; DB 1; Length 534;
 Best Local Similarity 47.4%; Pred. No. 2.6e-71;
 Matches 235; Conservative 84; Mismatches 149; Indels 28; Gaps 11;

QY 30 SINLTLSTDPSSIISAASHDFGNITVTTPGVICPSTADISRLQYAANGKS--TFQVAA 87
 DB 42 ALDGLRTDSNATAAASDFGNITSLPAVLYPSTADLVALLS-AANSTPGWPYTI 100

QY 79 GKSTFQVAARGQGHSLNGQASVGGVIVNMTCITDVVVKDKKYADVAAGTLWVDVLKKT 138
Db 61 G---LEISVRSGGHNPNGYATNDGGIVLDLRLMNSIHIDTAGSRARIGGGVSGDLVKEA 117
QY 139 AEKGVSPVSWTDYLHITVG--GTLNNGGIGGQVFRNGPLVSNVLELDVITKGEMLTCSR 196
Db 118 AKFGLAAVTG--MHPKVGFGLALNGGVGFLTPKYGLASDNILGATLVATGDIYICSD 174
QY 197 QLNPELFYGVGLGQFGIITRARIIVLDHAPKRAKWFRLYSDFTTFTKQDERLISMAND 256
Db 175 DERPELFWAVRGAGNFGVTEVEVQLYELP-----RKMLAGFITWAPSVSELAGLITS 228
QY 257 IGVVDLEGQIFLSNGVVD---TSRFPSPDQSKVADLVKQHGIIYVLEVAK 303
Db 229 L-LDAL-----NEMADHIYPSVFVGVDENRAPSVTVCVGHGLGLDIAE 270

RESULT 8
GGLO RAT STANDARD; PRT; 439 AA.
AC P10867; Q64597;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-gulonolactone oxidase (EC 1.1.3.8) (LGO) (L-gulono-gamma-lactone oxidase) (GLO).
GN GULO.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88115275; PubMed=3338984;
RA Koshizaka T., Nishikimi M., Ozawa T., Yagi K.;
RT "Isolation and sequence analysis of a complementary DNA encoding rat liver L-gulono-gamma-lactone oxidase, a key enzyme for L-ascorbic acid biosynthesis."
RL J. Biol. Chem. 263:1619-1621(1988).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=93016162; PubMed=1400507;
RA Nishikimi M., Kawai T., Yagi K.;
RT "Guinea pigs possess a highly mutated gene for L-gulono-gamma-lactone oxidase, the key enzyme for L-ascorbic acid biosynthesis missing in this species."
RL J. Biol. Chem. 267:21967-21972(1992).
CC -!- FUNCTION: Oxidizes L-gulono-1,4-lactone to hydrogen peroxide and L-xylono-1,4-lactone which spontaneously isomerizes to L-ascorbate.
CC -!- CATALYTIC ACTIVITY: L-gulono-1,4-lactone + O(2) = L-xylono-1,4-lactone + H(2)O(2).
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: Ascorbate biosynthesis; last step.
CC -!- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked oxidoreductase family.
CC -!- SIMILARITY: SOME, TO YEAST D-LACTATE DEHYDROGENASE [CYTOCHROME].
CC
CC
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CC
CC
CC EMBL; J03536; AAA41164.1; -.
DR EMBL; D12754; BAA02232.1; -.
DR EMBL; D12744; BAA02232.1; JOINED.
DR EMBL; D12745; BAA02232.1; JOINED.

DR EMBL; D12746; BAA02232.1; JOINED.
DR EMBL; D12747; BAA02232.1; JOINED.
DR EMBL; D12748; BAA02232.1; JOINED.
DR EMBL; D12749; BAA02232.1; JOINED.
DR EMBL; D14564; BAA02232.1; JOINED.
DR EMBL; D12750; BAA02232.1; JOINED.
DR EMBL; D12751; BAA02232.1; JOINED.
DR EMBL; D12752; BAA02232.1; JOINED.
DR EMBL; D12753; BAA02232.1; JOINED.
DR PIR; A45123; OXRTGU.
DR InterPro; IPR007173; ALO.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF04030; ALO; 1.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; 1.
KW Oxidoreductase; Flavoprotein; FAD; Ascorbate biosynthesis; Microsome; Transmembrane.
FT INIT_MET 0
FT BINDING 53 53 FAD (COVALENT) (BY SIMILARITY).
FT TRANSMEM 250 272 POTENTIAL.
FT CONFLICT 188 188 Q -> H (IN REF. 2).
FT CONFLICT 403 403 Q -> R (IN REF. 2).
SQ SEQUENCE 439 AA; 50475 MW; 79C08C26D31E8319 CRC64;
Query Match 6.5%; Score 169; DB 1; Length 439;
Best Local Similarity 19.6%; Pred. No. 0.00031;
Matches 96; Conservative 73; Mismatches 174; Indels 148; Gaps 17;
QY 63 PSSTADISRLLOVAANGKSTFQVAARGQGHSLNGQASVGGVIVNMTCITDVV-VSKDKK 121
Db 26 PTSVEEVREVLALAREQKKVKV--GGHS-PSDIACDTGFMTHMKMNRVLQVDKEKK 82
QY 122 YADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNG---GIGGQVFRNGPLVS 177
Db 83 QITVEAGILLADLHPQLDEHGLAMNLGAVSDVTVAGVIGSGTHNTGI-----KHGILAT 137
QY 178 NVLELDVITKGEMLTCSRQLNPELFYGVGLGQFGIITRARI----- 221
Db 138 QVVALTMTADGEVLECSERNADVFQAAARVHGLGCLGIILTVTLQCVQFQLQETSPST 197
QY 222 ---VLDHAP---KRAKWFRLYSDFT-----TFTKQERLISMANDIGVDYLEGQIFLSN 270
Db 198 LKEVLDNLDLHSLKSEYFRFLWFPHTENVSIYQDHTNKA PSSASNWFWDYAIG----- 251
QY 271 GVVDTSFFPPSDQSKVADLVKQHGIIYVLEVAKYVDDPNLPIISKVIDTLTKTSLYLP-- 328
Db 252 -----FYLLEF-----LLWTSTYLPCL 268
QY 329 -GFIS-----MHDVAYFDLNRVHVEENKLSGLWELP-HPWLNLYV 369
Db 269 VGWINRFFFWMLFNCKESSNLSHKIFTYECPKQHVQD-----WAIPREKTKEALL 320
QY 370 PKSRILDFHNGVVKDILLKQKSASGLALLYPTRNKNWDRMSAMIPEIDEDVIYIIGLLQ 429
Db 321 ELKAMLEAHPKVVAHYVVEVRFTRGDDIL-----LSPCFQDSCYMNIMY 366
QY 430 SATPKDLPESVNEKIIRFCCKDSGKIKIKQYLMHYTSKEDWIEHFGSKWDDFSKRKDLF- 488
Db 367 RPYGKDVPRL-----DYWLAYETIMKKFGGRPHWAKAHNCTQKDFEEMYPFTFH 414
QY 489 ---DPKKLLSP 496
Db 415 KFCDIKEXLDP 425
RESULT 9
RETO PAPSO
ID RETO PAPSO STANDARD; PRT; 535 AA.
AC P93479;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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	Query Match	5.9%;	Score 153.5;	DB 1;	Length 447;
	Best Local Similarity	27.5%;	Pred. No. 0.0036;		
	Matches 46;	Conservative 31;	Mismatches 85;	Indels 5;	Gaps 2;
QY	57	PGGVICPSS	TADISRLQLQYAANGKSTTFQVAARGQGHSLSLNGQASVSGGVIVNMTCTITDVVV	116	
		: :	: : :	: :	:
Db	30	PAYVEAADEQEVA	AARVLAAEFQKRPVGVMATGHGPSV----	SADDAVLVNTRRMEGSV	85
		: :	: : :	: :	:
QY	117	SKDKKYADVAGTLW	DVLDVKKTAEKGVSVPVSWTDYLHITVGGTSLNSGGIGGQVFNRGNPLV	176	
		: :	: :	: :	:
Db	86	DAARATAWIEAGAR	WRKVLEHTAPHGLAPLNSS-PNVGAUGLYLVGGAGLLGRFRFGYAA	144	
		: :	: :	: :	:
QY	177	SNVLELDVITKGEM	LTCRSQNLNPFLFYGLVGLGQFQGIITRARI VL	223	
		: :	: :	: :	:
Db	145	DHVRRRLRVTA	DGRLRDVTAGTDPDLFWAVRGGKDNFGLVVGMEVDL	191	
		: :	: :	: :	:

	Query Match	5.9%;	Score 153;	DB 1;	Length 439;
	Best Local Similarity	19.5%;	Pred. No. 0.0038;		
	Matches	92;	Conservative	83;	Mismatches 188; Indels 108; Gaps 19;
QY	63	PSSTADISRLQLVAAANGKSTFQVAAARGQGHSLNGQASVGGVIVNMTCTITDVV-VSKDKK	121		
Db	26	PTSVGEVREVLARQONKKVKV--GGGHS-PSDIACDGFMIHMGQNRVLQVDKEKK	82		
QY	122	YADVAAGTLWVDVLKTAEGVSPVSWTDYLTHTVGGTSLNG---GIGGOVFRNGPLVS	177		
Db	83	QVTVEAGILLTDLHPQLDKHGLALSNLGAVSVDVTGGVIGSGTHNTGI-----KHGILAT	137		
QY	178	NVLELDVITKGEMLTCSRQLNPFLFYGLGGLGQFGITTRARIVLDHAPKRAKWFRLY	237		
Db	138	QVVALTLMKADGTVLECSSESKADVFAARVHLGCLGVI--LTVTLCQVPQ----FHLLE	191		
QY	238	SDFTTFTKQERLISMANDIGVDYLEGQI-----FLSNGVVDTSFPPSDQSKVADLV	290		
Db	192	TSFPSTLKEV-----LDNLDShLKKSEYFRFL-----WFPHSE--NVSIY	230		
QY	291	KQGIIYVLEVAKYYDDPNLPIISKVIDTLTKTSLYP---GFIS-----	332		
Db	231	QDHNKEPSSASNWFD--YAIGFYLLLEFLLTWTSTYLPRLVGWINRFFFWLLFNCKESS	288		
QY	333	--MHDVAYDFLNRVHVEENKLRLSLGWELP-HPWLNLVYPKSRILDFHNGVVKDILLKQ	389		
Db	289	NLSHKIFSIECRFKQHVQD-----WAIPREKTKEALLEKALMLAHPKVAHYHVPVEV	340		
QY	390	KSASGLALLYPTNRNKNWDRMSAMIPEIDEDVIYIIGLLQSATPKDLPEVESVNEKIIRF	449		
Db	341	RFRGGDIL-----LSPCFQORDSCYNNIIMYRPGKDVPRL-----	376		
QY	450	CKDSGKIKQYLMHYTSKEDWIEHFGSKWDDFSKRKDLF----DPKKLLSP	496		
Db	377	--DYWLAYETIMKKFGGRPHWAKAHNCTRKDFEKMYPAFHKKFCDIREKLDP	425		

human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

FUNCTION: Oxidizes L-gulonono-1,4-lactone to hydrogen peroxide and L-xylono-1,4-lactone which spontaneously isomerizes to L-xylulose (By similarity).

CATALYTIC ACTIVITY: L-gulonono-1,4-lactone + O(2) = L-xylono-1,4-lactone + H(2)O(2).

COFACTOR: FAD (By similarity).

PATHWAY: Ascorbate biosynthesis; last step.

SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane (By similarity).

SIMILARITY: Belongs to the oxygen-dependent FAD-linked oxidoreductase family.

SIMILARITY: SOME, TO YEAST D-LACTATE DEHYDROGENASE [CYTOCHROME].

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RESULT 12
RETO_ESCCA
ID RETO_ESCCA STANDARD; PRT; 538 AA.
AC P30986;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Reticuline oxidase precursor (EC 1.21.3.3) (Berberine-bridge-forming
DE enzyme) (BBE) (Tetrahydroprotoberberine synthase).
GN BBE1.
OS Eschscholzia californica (California poppy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Papaveraceae; Eschscholziaceae; Eschscholzia.
OX NCBI_TaxID=3467;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP
RX MEDLINE=92052284; PubMed=1946465;

```

RA Dittrich H., Kutchan T.M.;
RT "Molecular cloning, expression, and induction of berberine bridge
RT enzyme, an enzyme essential to the formation of benzophenanthridine
RT alkaloids in the response of plants to pathogenic attack."
RL Proc. Natl. Acad. Sci. U.S.A. 88:9969-9973(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98145481; PubMed=9484487;
RA Hauschild K., Pauli H.H., Kutchan T.M.;
RT "Isolation and analysis of a gene bbel encoding the berberine bridge
RT enzyme from the California poppy Eschscholzia californica";
RL Plant Mol. Biol. 36:473-478(1998).
CC -!- FUNCTION: Essential to the formation of benzophenanthridine
CC alkaloids in the response of plants to pathogenic attack.
CC Catalyzes the stereospecific conversion of the N-methyl moiety of
CC (S)-reticuline into the berberine bridge carbon of (S)-scoulerine.
CC -!- CATALYTIC ACTIVITY: (S)-reticuline + O(2) = (S)-scoulerine +
CC H(2)O(2).
CC -!- COFACTOR: FAD and metal ion.
CC -!- PATHWAY: Benzophenanthridine alkaloids biosynthesis.
CC -!- SUBCELLULAR LOCATION: VESICULAR.
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S65550; AAB20352.1; -;
DR EMBL; AF005655; AAC39358.1; -;
DR PIR; A41533; A41533.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR InterPro; IPR006093; Oxid_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; 1.
KW Oxidoreductase; Signal; Glycoprotein; Flavoprotein; FAD;
KW Alkaloid metabolism.
FT SIGNAL 1 23
FT CHAIN 24 538 RETICULINE OXIDASE.
FT BINDING 104 104 FAD (COVALENT) (BY SIMILARITY).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 538 AA; 59958 MW; 1A505F86A06CDB24 CRC64;

Query Match 5.7%; Score 149; DB 1; Length 538;
Best Local Similarity 20.0%; Pred. No. 0.0095;
Matches 106; Conservative 89; Mismatches 181; Indels 154; Gaps 25;

QY 49 FGNITVTGGVICPSSSTADISRLQVAANGKSTFQVAARGQGHSLNGQASVSGG--VIV 106
Db 63 FQNSLISKPSAIIIPGSKELSNTIRCIRKGSWTIRL--RSGGHSYEGLSYTSPTFFILI 120
QY 107 NWTCTIDVVVSKDKYADVAAGT---LWVDVLKKTAEKGVSPVSWTDYHLHITVGGTLSN 162
Db 121 DLMNLRVSIIDLESETAWVESGSTLGELYVAITESSKLGFT-AGWCP--TVGTGGHISG 177
QY 163 GGIGGQVFRNGPLVSNVLELDVITGKGEMLTCSRQ-LNPELFYGV-LGGLGQFGIITRAR 220
Db 178 GGFGMMSRKYGLAADNVVDAILIDANGAIL--DRQAMGEDVFWAIRGGGGVWGAIIYAWK 235
QY 221 IVLDHAPKRAKWRFM-----LYSDFTTFT---KDQERL-ISMA 254
Db 236 IKLLVPPEKVTVFRVTKNVAIDEATSLHLKQWQFAEELEEDFTLSVLGGADEKQVWLTM 295
QY 255 N-----DIGV---DYLE---GQIFLSNGVVDT-----SFFPPS 281
Db 296 GFHFGKTVAKSTFDLLPPELGLVEEDYLEMSWGESFAYLAGLETVSQLNNRFLKFDERA 355

QY 282 DQSKVADLVKQHGIYVLEVAKYYDDPNLPISKVIDTTLTKLSYLP-GFISMHDVAYFD 340
Db 356 FKTKV-DLTKE-----PLPSKAFYGLLERLSKEPNGFIA----- 388
QY 341 FLNRVHVEENKLRSLGLWELPHLPWNLVYVPSKRILDFHNGVVVDILLKQKSASGLALLYP 400
Db 389 -LNGFGGQMSKISS-DFTPPH-----RSGTRLMVEYI 419
QY 401 TNRNKWDNRMSAMPEIDEDVIYIIGLQSATPK-----DLPEVESVNEKIIRFCK 451
Db 420 VAWNQSEQKKKTEFLDWLEKVEFMKPFVSKNPRGLGVNHHIDLDLGGIDWGNKTVV----- 475
QY 452 DSGIKIKQYLMHYTSKEDWIE-HFGSKWDDFSKRKDLFDPKKLLSPGQDI 500
Db 476 NNAIEISR-----SWGESYFLSNYERLIRAKTLIDPNNVFNHPQSI 516

RESULT 13

XYOA_STRCO
ID_XYOA_STRCO STANDARD; PRT; 418 AA.
AC Q9ZBU1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable xyloitol oxidase (EC 1.1.3.41).
GN XYOA OR SCO6147 OR SCLA9.11C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Harris D.E., Quail M.A., Kieser H.,
RA Thomson N.R., James K.D., Brown S., Chandra G., Chen C.W., Collins M.,
RA Harper D., Bateman A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Cronin A., Fraser A., Lark L., Murphy L., Oliver K., O'Neill S.,
RA Huang C.-H., Kieser T., Lark L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Taylor K.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: Catalyzes the oxidation of xyloitol to xylose, also acts
CC on D-sorbitol (By similarity).
CC -!- CATALYTIC ACTIVITY: Xylitol + O(2) = xylose + H(2)O(2).
CC -!- COFACTOR: FAD (By similarity).
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
CC

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EMBL; AL939126; CAA22381.1; -;
PIR; T34660; T34660.
InterPro; IPR006094; Oxid_FAD_bind.
InterPro; IPR006093; Oxid_FAD_BS.
Pfam; PF01565; FAD_binding_4; 1.
PROSITE; PS00862; OX2_COVAL_FAD; FALSE NEG.
KW Oxidoreductase; Flavoprotein; FAD (COVALENT) (BY SIMILARITY).
FT BINDING 46 46 FAD (COVALENT) (BY SIMILARITY).
SQ SEQUENCE 418 AA; 44346 MW; 2A80DF7735A87DCD CRC64;

Query Match 5.7%; Score 148; DB 1; Length 418;
Best Local Similarity 27.9%; Pred. No. 0.0079;

Search completed: April 5, 2004, 17:44:40
Job time : 20 secs

OM protein - protein search, using sw model

Run on: April 5, 2004, 17:41:36 ; Search time 46 Seconds
(without alignments)
3436.405 Million cell updates/sec

Title: US-10-014-101-4
Perfect score: 2596
Sequence: 1 MANLRMITLITVLMTKSS.....SKRKDLFDPKKLLSPGQDIF 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1221	47.0	536	10 Q9FE45	Q9fe45 dendrobium
2	1178	45.4	540	10 Q9FUJ0	Q9fujo arabidopsis
3	1102	42.4	532	10 Q8LJ52	Q8lj52 oryza sativ
4	1091	42.0	558	10 Q94IV9	Q94iv9 oryza sativ
5	1079	41.6	512	10 Q9FWT3	Q9fw3 arabidopsis
6	1063.5	41.0	525	10 Q8S0F8	Q8s0f8 oryza sativ
7	1060	40.8	526	10 Q8H6F6	Q8h6f6 hordeum vul
8	1056.5	40.7	575	10 Q22213	Q22213 arabidopsis
9	1054.5	40.6	520	10 Q84U27	Q84u27 hordeum vul
10	1054	40.6	526	10 Q8S394	Q8s394 hordeum vul
11	993	38.3	504	10 Q9LY71	Q9ly71 arabidopsis
12	991.5	38.2	527	10 Q8LNV6	Q8lnv6 oryza sativ
13	961	37.0	524	10 Q9FUJ1	Q9fu1 arabidopsis
14	928.5	35.8	532	10 Q7XKG2	Q7xkg2 oryza sativ
15	498	19.2	458	2 Q84HB2	Q84hb2 streptomyce
16	429	16.5	447	16 Q8YZY0	Q8yzy0 anabaena sp

17	387.5	14.9	137	10 Q94KI5	Q94ki5 triticum ae
18	376.5	14.5	137	10 Q94KI4	Q94ki4 hordeum vul
19	226.5	8.7	515	16 Q8NSU5	Q8nsu5 corynebacte
20	214	8.2	459	2 Q8GAG1	Q8gag1 arthrobacte
21	206.5	8.0	479	16 Q987W9	Q987w9 rhizobium l
22	202	7.8	464	2 Q9KHK2	Q9khk2 streptomyce
23	200	7.7	509	16 Q98I12	Q98i12 rhizobium l
24	196.5	7.6	466	16 Q8VIU9	Q8viu9 mycobacteri
25	196.5	7.6	470	16 Q69686	Q69686 mycobacteri
26	196.5	7.6	470	16 Q7TVU9	Q7tvu9 mycobacteri
27	196	7.6	479	16 Q92U94	Q92u94 rhizobium m
28	196	7.6	587	10 Q9SLW6	Q9slw6 nicotiana t
29	195	7.5	511	3 Q9P6Z1	Q9p6z1 neurospora
30	194	7.5	587	10 Q9FXL9	Q9fxl9 nicotiana t
31	193.5	7.5	469	16 Q8RD26	Q8rd26 thermoanaer
32	192.5	7.4	500	16 Q8F4R3	Q8f4r3 leptospira
33	192	7.4	461	16 Q87IH1	Q87ih1 vibrio para
34	192	7.4	588	10 Q8LP11	Q8lp11 lycopersico
35	185	7.1	439	16 Q82KJ4	Q82kj4 streptomyce
36	184	7.1	469	16 Q896M6	Q896m6 clostridium
37	183.5	7.1	459	16 Q69516	Q69516 mycobacteri
38	182	7.0	581	10 Q9ZMJ1	Q9zwm1 ipomoea bat
39	181.5	7.0	460	17 Q8PXD0	Q8pxd0 methanosarc
40	181.5	7.0	481	16 Q8F0N1	Q8f0n1 leptospira
41	181	7.0	503	17 Q8TH91	Q8th91 methanosarc
42	181	7.0	532	10 Q9FKV2	Q9fkv2 arabidopsis
43	179	6.9	453	16 Q82CC8	Q82cc8 streptomyce
44	178	6.9	472	2 Q9X5T1	Q9x5t1 streptomyce
45	178	6.9	488	16 Q8NTW2	Q8ntw2 corynebacte

ALIGNMENTS

RESULT 1
Q9FE45 ID Q9FE45 PRELIMINARY; PRT; 536 AA.
AC Q9FE45;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytokinin oxidase.
GN CKO1.
OS Dendrobium cv. 'Sonia'.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Dendrobieae; Dendrobieinae;
OC Dendrobium.
OX NCBI_TaxID=136995;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang S., Yu H., Goh C.;
RT "Molecular cloning and characterization of a cDNA encoding cytokinin
oxidase in Dendrobium sonia orchid."
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ294543; CAC17753.1; -.
DR EMBL; AJ294542; CAC17752.1; -.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF01565; FAD_binding_4; 1.
SQ SEQUENCE 536 AA; 60386 MW; ACDF30A77BC940AE CRC64;

Query Match 47.0%; Score 1221; DB 10; Length 536;
Best Local Similarity 47.9%; Pred. No. 9.9e-80;
Matches 252; Conservative 82; Mismatches 162; Indels 30; Gaps 11;

QY	3	NLRMITLI--TVLMTKSNIGIKIDLPKSLNLTLDPS-----IISAASHDFGN 51
Db	2	NLHAMPPFLNPTSLLLTTLTMSILIQSPNSLPTNLLTHTSTHLRFDLSLSAASSDFGD 61
QY	52	ITTVTPGGVICPSSTADISRLQYAANGKSTFQVAARGQCHSLNGQASVSGGVIWNMTCI 111
Db	62	IIHSLPSAVFLPSSPSDIATLLRLSHFSPHSFTVSARGLGHSTRGQAQAFGGIVINMPSL 121

QY	112	T-DVVVSKKKYADVAAGTLWVDVLKKTABKGVSPVSWTDYLIHITVGGTSLNGGIGQVF	170
Db	122	DGGITVSDGMFVDACAEQMWIDVLRHGLTPKSWTDYLYLTGGLTSLNGGIGSQAF	181
QY	171	RNGPLVSNVLELDVITGKGEMLTCSRQLNPFLFYGLGGLGQFGIITRARIIVLDHAPKRA	230
Db	182	LHGPQISNVHELIDVITGKGEMVTCSESNNPDLFFSVLGGGLGQFGIITRARIALEKAPQSV	241
QY	231	KWFRMLYSDEFTTFTKQERLISM-ANDIG--VDYLEGQIFLSNGVVD---TSFFPPSDQS	284
Db	242	RWMRLMYTDFELFTKQELLISIKAEGBGKLVNVEGSLLMHESLSKNWRSPPFFSEKDLK	301
QY	285	KVADLVK-QHGIIYVLEVAKYD---DPNLPIISKV-----IDTLTKLSYLPFGFISMHD	335
Db	302	KIKKLASGNEGVIIYCLEASFYDYGHENMFNRADKAQMDQDIEELLRLKLSFVSGFAFRND	361
QY	336	VAYDFLNRVHVEENKLSGLWELPHWPNLVVPKSRILDFHNGVVDKILLKQKSASGL	395
Db	362	VSYMFLNRVHDGELKLRAMGLWDVPHWPNLVFVSKSNIMDFHIGVFKGIMKNKS-MGP	420
QY	396	ALLYPTNRNKNWNRMSAMIDEDEDVIYIIGLQSAATPKDLPESVNEKIIRFCKDSGI	455
Db	421	ILVYPTKRKWKDCKRMSTSP--DEEVFYSIGILLSSEMNDLEHLESHNAEILKFCDDQGM	478
QY	456	KIKQYLMHYTSKEDIHFGSKWDDFSKRKXOLFDPKLLSPGQDIF	501
Db	479	NYKQYLPHYTSEDWKXGFGKWERFVEMKSRYPDKAILSPGQKIF	524
RESULT 2			
Q9FUJ0			
ID	Q9FUJ0	PRELIMINARY;	PRT; 540 AA.
AC	Q9FUJ0;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Cytokinin oxidase.		
GN	CKX6.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Bilyeu K.D., Laeky J.G., Riekhof W.R., VanVickle S., Morris R.O.;		
RT	"A family of cytokinin oxidases from Arabidopsis thaliana.";		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF303982; AAC30909.1; --		
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR006094; Oxid_FAD_bind.		
DR	InterPro; IPR006093; Oxred_FAD_BS.		
DR	Pfam; PF01565; FAD_binding_4; 1.		
DR	PROSITE; PS00862; OX2_COVAL_FAD; 1.		
SQ	SEQUENCE 540 AA; 60389 MW; D74DD0D50CEBA76F CRC64;		
Query Match 45.4%; Score 1178; DB 10; Length 540;			
Best Local Similarity 48.6%; Pred. No. 1.3e-76;			
Matches 232; Conservative 84; Mismatches 143; Indels 18; Gaps 7;			
QY	39	PSIIISAASHDFGNI-TTVPGGVICPSTADISRLQYAANGKSTFQVAARGQHSLNGQ	97
Db	48	PSDLASVSSDFGMLKSPEEPLAVLHPSSAEDVARLVRTAYGSAFAPVVSARGHGSINGQ	107
QY	98	ASVS-GGVIIVNM---TCITDVVSKDKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYL	152
Db	108	AAAGRGVVMVNMHGVGTGPKPLVRPDEMYVDVWGGELWVDVLKKTLEHGLAPKSWTDYL	167
QY	153	HITVGGTSLNGGIGQVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPFLFYGVGLGLGQ	212
Db	168	YLTVGGTSLNAGISQALHHGPQISNVLELDVVTGKGEVMRCSEENTRLFHGVGLGLGQ	227

QY	213	FGIITRARIIVLDHAPKRAKWRMLYSDEFTTFTKQERLISMANDIGVDYLEGQIFLSNGV	272
Db	228	FGIITRARIISLEPAPQRVRWIRVLYSSFKVFTEDQEYLISMHGQLKFDYVEGFVIVDEGL	287
QY	273	VD---TSFFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKTSLYLPG	329
Db	288	VNNWRSFFSPRNPVKISSVSSNGSVLYCLEITKNYHDSSEIVDQVEILMKKLNFIPT	347
QY	330	FISMHDVAYDFLNRVHVEENKLSGLWELPHWPNLVVPKSRILDFHNGVVDKILLKQ	389
Db	348	SVFTTDLQYVDFLDRVHKAELKLSKNLWEVPHWPNLVFVPKSRISDFDKGVFKGIL--G	405
QY	390	KSASGALLLYPTNRNKNWNRMSAMIDEDEDVIYIIGLQSA-----TPKDLPEVESVNE	444
Db	406	NKTSGPILIYPMNKDKWDERSSAVTP--DEEVYLVALLRSALTGDGEETQKLEYLKDQNR	463
QY	445	KIIRFCKDSGIIKQYLMHYTSKEDIHFGSKWDDFSKRKOLFDPKLLSPGQDIF	501
Db	464	RILEFCEQAKINVKQYLPHHATQEEWVAHFQDKWDRFRSLKAEFDPRHILATGQRIF	520
RESULT 3			
Q8LJ52			
ID	Q8LJ52	PRELIMINARY;	PRT; 532 AA.
AC	Q8LJ52;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Putative cytokinin oxidase.		
GN	P0413G02.1.		
OS	Oryza sativa (japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartioideae; Oryzeae; Oryza.		
OX	NCBI_TaxID=39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nipponbare;		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC		
RT	clone:P0413G02.";		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AP003344; BAC07345.1; --		
DR	Gramene; Q8LJ52; --		
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR006094; Oxid_FAD_bind.		
DR	InterPro; IPR006093; Oxred_FAD_BS.		
DR	Pfam; PF01565; FAD_binding_4; 1.		
DR	PROSITE; PS00862; OX2_COVAL_FAD; 1.		
SQ	SEQUENCE 532 AA; 58016 MW; C3B56144953DE2FF CRC64;		
Query Match 42.4%; Score 1102; DB 10; Length 532;			
Best Local Similarity 45.5%; Pred. No. 3.9e-71;			
Matches 222; Conservative 89; Mismatches 151; Indels 26; Gaps 9;			
QY	35	LSTDPSIIISAASHDFGNITTVPGGVICPSSSTADISRLQYAANGKSTFQVAARGQHSL	94
Db	41	LSVEPSDVMEASLDFGRLTSAEPLAVFHPRGAGDVAALVKAAYGSASGIRVSARGHHSI	100
QY	95	NGQASVSGGVIIVNMT-----CITDVVVSOKKYADVAAGTLWVDVLKKT-AEKGV	143
Db	101	SGQAQAAGGVVVDMSHGWRAEAAERTLPVYSPALGGHYIDVWGELWIDVLNWTLAHGGL	160
QY	144	SPVSWTDYLIHITVGGTSLNGGIGQVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPFL	203
Db	161	APRSWTDYLYSVGGTSLNAGISGQAFHHGPQISNVYELDVVT-KGEVVTCSSENNPDLF	219
QY	204	YGVGLGLGQFGIITRARIIVLDHAPKRAKWRMLYSDEFTTFTKQERLISMAN-DIGVDYL	262
Db	220	FGALGGLGQLGIITRARIALEPAPHRVRWIRALYSNFTFTADQERLISLQHGRRRFDYV	279

QY	263	EGQIFLSNGVVD--TSFFPPSDQSKVADLVKQHGIIYVLEVAKYYDDPNLPIISKVIDT	319
Db	280	EGFVAAEGLNNWRSFFSPQNPVKLSLKHSGVLVCLVTKNYDDSTAVTDQDVEA	339
QY	320	LTKTLSYLPGFISMHDVAYDFLNRVHVEENKLRSLGLWELPHLPWLNLYVPKSRILDFHN	379
Db	340	LLGELNFIPGTVFTTDLPLYVDFLDRVHKAELKLRGKGMWEVPHLPWLNLFVPASRIADFR	399
QY	380	GVVKDILLKQKSASGLALLYPTNRNKNWNRMSAMIPEDIDEDVIYIIGLLQSATP-----	433
Db	400	GVFRGV-LGSRTAGGPILYPMNRH-WDPRSSVVTPE--EDVYLVAFLSRAVPGSTDPA	455
QY	434	KDLPEVESVNEKIIRFKDSGKIKQYLMHYTSKEDWIEHFGSKWDDFSKRKDLDFDPKXL	493
Db	456	QSLEALERQNRREILEFCDEAGIGAKQYLPNHNKQREWEAHFGARWARPARLKAEFDPGRAM	515
QY	494	LSPGQDIF 501	
Db	516	LATGQGIF 523	
RESULT 4			
Q94IV9	PRELIMINARY; PRT; 558 AA.		
ID	Q94IV9		
AC	Q94IV9;		
DT	01-DEC-2001 (TReMBLrel. 19, Created)		
DT	01-DEC-2001 (TReMBLrel. 19, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	Putative cytochrome oxidase.		
GN	P0419B01.11 OR B1046G12.5.		
OS	Oryza sativa (Rice), and		
OS	Oryza sativa (japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzeae; Oryza.		
OX	NCBI_TaxID=4530, 39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nipponbare;		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC		
RT	clone:P0419B01.1";		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nipponbare;		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC		
RT	clone:B1046G12.1";		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AP003244; BAB56095.1; -.		
DR	EMBL; AP003200; BAB89407.1; -.		
DR	Gramene; Q94IV9; -.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR006094; Oxid_FAD_bind.		
DR	Pfam; PF01565; FAD_binding_4; 1.		
SQ	SEQUENCE 558 AA; 59121 MW; B3472B591AD1EFF7 CRC64;		
Query Match 42.0%; Score 1091; DB 10; Length 558;			
Best Local Similarity 45.3%; Pred. No. 2.6e-70;			
Matches 233; Conservative 91; Mismatches 142; Indels 48; Gaps 12;			
QY	35	LSTDPSIIISAASHDFGNITVTPG-----GVICPSSTADISRLLQYAANGKSTFQVA	86
Db	41	IRADEAGTARASADFNLVAGVAPRLAAAALYPSRPADIAALLRASCARPAPAVS	100
QY	87	ARGQGHSLNGQASVSGGVIVNMTCI-----TDVVVSKDKKYADVAAGTLWVDVLKKT	138
Db	101	ARGCGHSHVHQASAPDGVVVDMAISLGRLLQGGARRLAVSVGRIYVDAGGEQLWVDVLRA	160
QY	139	AEKGVSPVSWTDYLIHTVGGTSLNGGIGGQVFRNGPLVSNVLELDVITGKGMELTCSRQL	198
Db	161	MAHGLTPVSWTDYLIHTVGGTSLNAGISQAFRHGPQISNVLELDVITGVGMVTCSEK	220

QY	199	NPELFYGVGLGQFGIITRARIIVLDHAPKRAKWRMLYSDFITFTTKDQERLISM-----	253
Db	221	APDLFVGLGQFGVITRARIPLAPAPARARWRFVYTTAAAMTADQERLIAVDRAAG	280
QY	254	ANDIG--VDYLEGQIFLSNGVVDT-----SFFPSPDQSKVADLVKQ-HG	294
Db	281	AGAVGGLMDYVEGSHVHLNQGLVETWRTQPPSPSSSSSSSSSSSSSSSSSSSSSSSSSS	340
QY	295	IIVLEVAKYYD---DPNLPISKVIDTLTKTLSYLPGFISMHDVAYDFLNRVHVEENK	351
Db	341	VLYFLEGAIYFGGAAGPSAADVDKRMVDLRRRLRHERGFVFAQDVAYAGFLDRVHDGELK	400
QY	352	LRLSLWELPHLPWLNLYVPKSRILDFHNGVVVKDILLKQKSASGLALLYPTNRNKNWNRMS	411
Db	401	LRAAGLWDVPHLPWLNLFPRSGVLAFAADGVFHGI-LSRTPAMGVPVLIYPMNRNKNWDSNMS	459
QY	412	AMIPEID-EDVIYIIGLLQSATPK-DLPEVESVNEKIIRFKDSGKIKIKQYLMHYTSKED	469
Db	460	AVITDDDGDEVFTVGIILRSAAAAGDVGRLEEQNDLILGCEVAGIAYKQYLPYYSQAE	519
QY	470	WIE-HFGSK-WDDFSKRKDLDFPKLLSPGQDIF 501	
Db	520	WQKRHFGANLWPRFVQRKSKYDPAKILSRGQGIF 553	
RESULT 5			
Q9FWT3	PRELIMINARY; PRT; 512 AA.		
ID	Q9FWT3		
AC	Q9FWT3;		
DT	01-MAR-2001 (TReMBLrel. 16, Created)		
DT	01-MAR-2001 (TReMBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	F1B16.2 protein.		
GN	F1B16.2.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,		
RA	Altati H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,		
RA	Buehler E., Chao Q., Chin C., Chio J., Choi E., Gonzalez A.,		
RA	Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,		
RA	Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,		
RA	Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AC023754; AAG13068.1; -.		
DR	PIR; B96785; B96785.		
DR	GO; GO:0005622; C:intracellular; IEA.		
DR	GO; GO:0005840; C:ribosome; IEA.		
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.		
DR	GO; GO:0003735; F:structural constituent of ribosome; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	GO; GO:0006412; P:protein biosynthesis; IEA.		
DR	InterPro; IPR006094; Oxid_FAD bind.		
DR	InterPro; IPR006093; Oxred_FAD_BS.		
DR	InterPro; IPR002132; Ribosomal_L5.		
DR	Pfam; PF01565; FAD_binding_4; 1.		
DR	PROSITE; PS00862; OX2_COVAL_FAD; 1.		
DR	PROSITE; PS00358; RIBOSOMAL_L5; 1.		
SQ	SEQUENCE 512 AA; 57292 MW; 4CA5B3F93EEFDA51 CRC64;		
Query Match 41.6%; Score 1079; DB 10; Length 512;			
Best Local Similarity 45.7%; Pred. No. 1.7e-69;			
Matches 218; Conservative 80; Mismatches 137; Indels 42; Gaps 8			
QY	39	PSIIISAASHDFGNI-TTVTPGGVICPSSTADISRLLQYAANGKSTFQVAARGQGHSLNGQ	97
Db	44	PSDLASVSSDFGMLKSPEEPLAVLHPSSAEDVARLVRTAYGSAFAPVSARGHGSINGQ	103

QY 98 ASVS-GGIVANM---TCITDVVSKDKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYL 152
Db 104 AAAGRNGVVMNMGVGTGTPKPLVRPDEMYYDVWVGELWVDVLKKTLEHGLAPKSWTDYL 163
QY 153 HITVGGTSLNGGIGGVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPBELFYGVGLGLGQ 212
Db 164 YLTVGGTSLNAGISGQAFHHGPQISNVLELDVVT-----GQ 199
QY 213 FGIITRARIIVLDHAPKRAKWFRLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGV 272
Db 200 FGIITRARIISLEPAPQVRWIRVLYSSFKVFTEDEQYELISMHGQLKFDYVEGFVIVDEGL 259
QY 273 VD---TSFFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKLSYLP 329
Db 260 VNNWRSFFSPRPVKISSVSSNGSVLYCLEITKNYHDSDEIVDQVEIIMKKNFIPT 319
QY 330 FISMHDVAYFDLNRVHVEENKRLSLGLWELPHWPNLNVVPKSRILDFHNGVVKDILLKQ 389
Db 320 SVFTTDLYVDLDRVHKAECLKRSKNLWEVPHWPNLNVFPKSRISDFDKGVFKGIL--G 377
QY 390 KSASGLALLYPTRNNKWDNRMSAMIPEIDEDVIYIIGLLQSA-----TPKDLPEVESVNE 444
Db 378 NKTSGPILIYPMNKDKWDRSSAVTP--DEEVFYLVALRLRSALTGDGEETQKLEYLKDQNR 435
QY 445 KIIRFCKDSGIKIKOYLMHYTSKEDWIEHFGSKWDDFSKRKDLDFDPKLLSPGQDIF 501
Db 436 RILEFCEQAKINVKOYLPHPHATQEEWVAHFQKWDREPSLKAEFDPRHILATGQRIF 492

RESULT 6
Q8SOF8
ID Q8SOF8 PRELIMINARY; PRT; 525 AA.
AC Q8SOF8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative cytokinin oxidase.
GN B1150F11.19.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC clone:B1150F11."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003412; BAB90259.1; -.
DR Gramene; Q8SOF8; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; 1.
SQ SEQUENCE 525 AA; 58011 MW; D10B03BFD4259DDD CRC64;

Query Match 41.0%; Score 1063.5; DB 10; Length 525;
Best Local Similarity 43.3%; Pred. No. 2.3e-68;
Matches 205; Conservative 94; Mismatches 153; Indels 21; Gaps 8;
QY 44 AASHDFGNITVTTPGVICPSSTADISRLQ--YAANGKSTFQVAARGQGHSLNGQASVS 101
Db 50 AAARDFGNRCSLPAAVLHPGSVSDVAATVRVVFQGRSSPLTVAARGHSHLLGQSQA 109
QY 102 GGIVNMTCTIDV-----VVKDKKYADVAACTLWVDVLKKTAEKGVSPVSWTDYLHIT 155
Db 110 GGIVVKMESLAAAAARAVRHGGASPHVDAPGGELWINVLHETLKHGLAPRSWTDYLHT 169
QY 156 VGGTSLNGGIGGVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPBELFYGVGLGLGQFGI 215

Db 170 VGGTSLNAGVSGQAFRHGPQVSNVNQLEIVTGRGEVVTCSHEVNSDLFYAALGGLGQFGI 229
QY 216 ITRARIIVLDHAPKRAKWFRLYSDFTTFTKQERLISMANDIGVDYLEGQIFLS-NGVVD 274
Db 230 ITRARIALEPAPKMWIRVLYSDFTFTDEQEKLI--ASEKTFDYIEGFVIINRTGILN 287
QY 275 T--SFFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKLSYLPGFIS 332
Db 288 NWRTSFKPQDPVQASQFQSDGRVLYCLELTMNHNHDEADIMEQEVGALLSRLRYISSTLF 347
QY 333 MHDVAYFDLNRVHVEENKRLSLGLWELPHWPNLNVVPKSRILDFHNGVVKDILLKQKSA 392
Db 348 YTDVTVYLEFLDRVHTSELKRAQGLWEVPHWPNLNLIPRSTVHKFAKEVFGKIL--KDSN 405
QY 393 SGLALLYPTRNNKWDNRMSAMIPEIDEDVIYIIGLLQSATPK---DLPEVESVNEKIIR 448
Db 406 NGPILLYPVNRTKWDNRTSVVIP--DEEIFYLVGFLSSAPSSSGHSGSVEHAMNLLNNKIYD 463
QY 449 FCKDSGIKIKOYLMHYTSKEDWIEHFGSKWDDFSKRKDLDFDPKLLSPGQDIF 501
Db 464 FCEKNGVGMKQYLAPTYTQKQWKAHFGARWETFERRKHTYDPLAILAPGQRIF 516

RESULT 7
Q8H6F6
ID Q8H6F6 PRELIMINARY; PRT; 526 AA.
AC Q8H6F6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytokinin dehydrogenase 2 (EC 1.5.99.12).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Luxor;
RA Galuszka P., Frebort I.;
RT "Cytokinin dehydrogenase genes in barley."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF540382; AAN16383.1; -.
DR GO; GO:0019139; F:cytokinin dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR InterPro; IPR006093; Oxred_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; 1.
KW Oxidoreductase.
SQ SEQUENCE 526 AA; 58848 MW; 9443FF33C75D2C2F CRC64;

Query Match 40.8%; Score 1060; DB 10; Length 526;
Best Local Similarity 42.2%; Pred. No. 4.2e-68;
Matches 215; Conservative 100; Mismatches 174; Indels 20; Gaps 10;
QY 6 LMITLITVLMITKSSNGIKIDLPKSLNLTSLTDPSI---ISAASHDFGNITVTTPGGVI 61
Db 9 LKLFLLLLGLGAVTAEHVLKHDVLASLG-TLPDGHFSFHDLSAAAMD FGNLSSFPFPAVL 67
QY 62 CPSSTADISRLQ--YAANGKSTFQVAARGQGHSLNGQASVSGGVNMTCTIDV---VV 116
Db 68 HPGSVADIATTVRHVFLMGEHSALTVAARGHSHLYGQSQAAGGIVIRMESLRSVKMQVH 127
QY 117 SKDKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLV 176
Db 128 PGASPYVDASGGELWINVLNKTLYGLAPKSWTDYLHITVGGTSLNAGVSGQTFRHGPQI 187
QY 177 SNVLELDVITGKGEMLTCSRQLNPBELFYGVGLGLGQFGIITRARIIVLDHAPKRAKWFRL 236
Db 188 SNVNELEIVTGRGDIVTCSPEQNSDLFRAALGGLGQFGIITRARIILEPAPQWVRWIRVL 247

Db 86 GEHSTLTVAARGHSHLYGQSOAAGGIVIRMESLQSVKMVHPGASPYVDASGGELWINV 145

QY 135 LKKTAEKGVSPVSWTDYHLHITVGGTSLNSGGIGGVFRNGPLVSNVLELDVITKGEMLTC 194

Db 146 LNKTLKYGLAPKSWTDYHLHITVGGTSLNAGVSGQTFRHGPQISNVNLEIIVTGRDIIITC 205

QY 195 SRQLNPFLFYVGLGQGFIIITRARIIVLDHAPKRAKWFRLYSDFTTKDQERLISMA 254

Db 206 SPEQNSDLFHAALGGLGQFGIITRARIALEPAPQMVWRWIRVLYLDFMSLTEDQEMLISAE 265

QY 255 NDIGVDYLEGQIFLS-NGVVDY--SFFPPSDQSKVADLVKQHGIIVYLEVAKYYDDPNLP 311

Db 266 KTF--DYIEGFVSINRTGILNNRSSFNPQDPERASQFETDRKVLFCLEMTKNF-NPEEA 322

QY 312 IISKVIDTLTKLSYLPGFISMHDVAYFDFLNRVHVEENKLSLGLWELPHPWNLNLYVPK 371

Db 323 GIMEQIHALLSQLRYTPPSLFHTDVTYMEFLDRVHSSSEIKRAKGLWEVHPWNLNLIIPR 382

QY 372 SRILDFHNGVVKDILLKQKSASGLALLYPTRNRKNWNRMSAMIPEIDEDVIYIIGLLQSA 431

Db 383 STVHTFAKQVFGKIL--EDNNGNPILLYPVNKSQRWNRTSVLP--DEEVSYLVGFLPSA 438

QY 432 T-PKDLPEVESVNEKIIIRFCKDSGIIKQYLMHYTSKEDWIEHFGSKWDDFSKRKDLFDP 490

Db 439 MGPHSIKRTLNLNNQIIIEFSNKASIGVKQYLPHYSTEPENKAHYGARWDAPQQRKNTYDP 498

QY 491 KKLLSPGQDIF 501

Db 499 LAILAPGORIF 509

RESULT 10

Q8S394

ID Q8S394 PRELIMINARY; PRT; 526 AA.

AC Q8S394

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Cytokinin dehydrogenase 2 (EC 1.5.99.12).

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;

OC Triticeae; Hordeum.

OX NCBI_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RA Galuszka P., Frebort I.;

RT "Cytokinin dehydrogenase genes in barley.";

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF490591; AAM08400.2; -

DR GO; GO:0019139; F:cytokinin dehydrogenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006094; Oxid_FAD_bind.

DR InterPro; IPR006093; Oxred_FAD_BS.

DR Pfam; PF01565; FAD_binding_4; 1.

DR PROSITE; PS00862; OX2_COVAL_FAD; 1.

KW Oxidoreductase.

SQ SEQUENCE 526 AA; 58814 MW; 97207FD3C090E62F CRC64;

Query Match 40.6%; Score 1054; DB 10; Length 526;

Best Local Similarity 42.0%; Pred. No. 1.1e-67;

Matches 214; Conservative 100; Mismatches 175; Indels 20; Gaps 10;

QY 6 LMITLITVLMITKSSNGIKIDLPKSLNLTLDPSI----ISAASHDFGNITVTTPGGVI 61

Db 9 LKFLLLGLGAVTAEHVVKHDLVSLG-TLPDGHFSFHDLSAAAMD FGNLSFPFPAVL 67

QY 62 CPSSTADISRLQ--YAANGKSTFQVAARGQHSHLNGQASVGGVIVNMTCTIDV---VV 116

Db 68 HPGSVADIATTVRHVFLMGEHSALTVAARGHSHLYGQSQAGGIVIRMESLRVKNQVH 127

QY 117 SKDKKYADVAACTLWVDVLKKTAEKGVSPVSWTDYHLHITVGGTSLNSGGIGGVFRNGPLV 176

Db 128 PCASPYVDASGGELWINVNLKTKYGLAPKSWTDYHLHITVGGTSLNAGVSGQTFRHGPQI 187

QY 177 SNVLELDVITKGEMLTCRQLNPFLFYVGLGQGFIIITRARIIVLDHAPKRAKWFRL 236

Db 188 SNVNELEIIVTGRDIVTCSPEQNSDLFRAALGGLGQFGIITRARIALEPAPQMVWRWIRV 247

QY 237 YSDFTTKDQERLISMANDIGVDYLEGQIFLS-NGVVDY--SFFPPSDQSKVADLVKQH 293

Db 248 YLDFMSLTEDQEMLISAEKTF--DYIEGFVILNRTGILNNRSSFNPQDPERASRFETDR 305

QY 294 GIIYVLEVAKYYDDPNLPILISKVIDTLTKLSYLPGFISMHDVAYFDFLNRVHVEENKLR 353

Db 306 KVLFCLEMTKNFNPPEADIMEQEVEHALLSQLRYTPASLFHTDVTYIEFLDRVHSEMMLR 365

QY 354 SLGLWELPHPWNLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTRNRKNWNRMSAM 413

Db 366 AKGLWEVHPWNLNLIIPRSTIHTFAEQVFGKIL--EDNNGNPILLYPVNKSQRWNRTSV 423

QY 414 IPEIDEDVIYIIGLLQSAT-PKDLPEVESVNEKIIIRFCKDSGIIKQYLMHYTSKEDWIE 472

Db 424 IP--DEEVFYLVGFLSSAIGPHSIEHTLNLNNQIIIEFSNKASIGVKQYLPNYTTEPEWKA 481

QY 473 HFSGKWDDFSKRKDLFDPKLLSPGQDIF 501

Db 482 HYGARWDAPQQRKNTYDPLAILAPGQKIF 510

RESULT 11

Q9LY71

ID Q9LY71 PRELIMINARY; PRT; 504 AA.

AC Q9LY71;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytokinin oxidase-like protein.

GN MAA21_70.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd S.;

RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL163818; CAB87797.1; -

DR PIR; T49185; T49185.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006094; Oxid_FAD_bind.

DR Pfam; PF01565; FAD_binding_4; 1.

SQ SEQUENCE 504 AA; 56519 MW; 203961A475847F8D CRC64;

Query Match 38.3%; Score 993; DB 10; Length 504;

Best Local Similarity 41.5%; Pred. No. 2.8e-63;

Matches 217; Conservative 100; Mismatches 152; Indels 54; Gaps 14;

QY 6 LMITLITVLMIT-----KSSNGIKIDLPKSLNLTLDPSIISAASHDFGNITTV 55

Db 2 LIVRSFTILLSCIAFKLACCFSSS-----ISSLKALPLVGHLEFEHVHASKDFGNRYQL 57

QY 56 TPGGVICPSTADISRLQ--YAANGKSTFQVAARGQHSHLNGQASVGGVIVNMTCTID 113

Db 58 IPLAVLHPRKSVSDIASTIRHIMMGTHSOLTVAARGRHSLQGQAQTRHGIVIHMESLHP 117

QY 114 -----VVVSKDKKYADVAAAGTLWVDVLKKTAEKGVSPVSWTDYHLHITVGGTSLNSGGIGGQ 168

Db 118 QKLQVSVDSPPAPYVDVSGGELWINILHETLKYGLAPKSWTDYHLHITVGGTSLNAGISGQ 177

QY 169 VFRNGPLVSNVLELDVITGKGMELTCSRQNLPELFGVGLGQFGIITRARIIVLDHAPK 228
 Db 178 AFRHGPOISNVHQLEIVTGKEILNCTKQNSDLFNGVLGGLGQFGIITRARIAPAP- 236
 QY 229 RAKWFRMLYSDFTTFTKDOERLISMANDIGVDYLEGQIFLS-NGVVDY- --SFFPPSDQS 284
 Db 237 -----TMDQEQQLS-AQGHKFDYIEGFVIINRTGLNSWRLSF--TAPEP 278
 QY 285 KVADLVKQHG-IIVVLEVAKYDDPNLPIISKVIDTLTKTLVLPFGFISMDHVAFFDLN 343
 Db 279 LEASQKFDGRTLYCLELAKYLKQDNKDVINQEVKETSLSVYVSTLFTTEVAYEARLD 338
 QY 344 RVHVEENKLSGLWELPHWPLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNR 403
 Db 339 RVHSEVLSKSGQWVPHWPLNLLVPSKINEFARGVFGNLL--TDTSGPVIVYPVVK 396
 QY 404 NKWDNRMSAMTPEIDEDVYIIGLLQSATP-----KD-LPEVESVNEKIIRFKDSGKIK 458
 Db 397 SKWDNQTSAVTPE--EEVYLVAILTSAPSGSAGKDVVEEILRRNRILFSEEGIGLK 454
 QY 459 QYLMHYTSKEDWIEHFGSKWDDFSKRDLPDPKLLSPGQDIF 501
 Db 455 QYLPHTTTRERNRSHFGDKWGEFVRRKRYDPLAILAPGHRIF 497

RESULT 12
 Q8LNV6 PRELIMINARY; PRT; 527 AA.
 ID Q8LNV6
 AC Q8LNV6;
 DT 01-OCT-2002 (TremBLrel. 22, Created)
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Putative cytochrome oxidase.
 GN OSUNBA0012L23.33.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
 RA Overton I.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
 RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
 RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
 RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
 RA "Oryza sativa chromosome 10 BAC OSUNBA0012L23 genomic sequence."
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA The Rice Chromosome 10 Sequencing Consortium;
 RA "In-depth view of structure, activity, and evolution of rice
 RT chromosome 10."
 RL Science 300:1566-1569(2003).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R., Ming R.A., McCombie W.R., Messing J., Yuan Q.,
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC051632; AAM91887.1; --
 DR EMBL; AE017106; AAP54326.1; --
 DR Gramene; Q8LNV6; --
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006094; Oxid_FAD_bind.
 DR Pfam; PF01565; FAD_binding_4; 1.
 DR SEQUENCE 527 AA; 58428 MW; 9EB8175695F49265 CRC64;

Query Match 38.2%; Score 991.5; DB 10; Length 527;
 Best Local Similarity 42.4%; Pred. No. 3.8e-63;
 Matches 211; Conservative 94; Mismatches 146; Indels 47; Gaps 14;

QY 31 LNLTLSTDPSSIISAASHDFGNITVTPGGVICPSSTADISRLQYAAAN---GKSTFQVAA 87
 Db 35 LNLTPTT-----TTASSDFGRILFHSPSAVLKQAPRDISLLSFLSASPLGKVT--VAA 87
 QY 88 RGQGHSLNGQASVSGGVIVNMTCTIDVVV-----SKKKYADVAAGTLVVDVLTAEKG 142
 Db 88 RGAGHSIHGOAALDGIIVVEMSSLPSEIEFYRRGEGDVSADVGGIMWIELLEQSLKLG 147
 QY 143 VSPVSWTDYLTHTVGGTSLNGGIGGVFRNGPLVSNVLELDVITGKGMELTCSRQNLPEL 202
 Db 148 LAPRSWTDYLTHTVGGTSLNAGISGQTFKHPQISNVLQLEVVITGRGEIVTCSPTKDAEL 207
 QY 203 FYGVGLGLGQFGIITRARIIVLDHAPKRAKWRMLYSDFTTFTKDOERLISMANDIGVDYL 262
 Db 208 FNAVGLGLGQFGIITRARIIVLDHAPKRAKWRMLYSDFTTFTKDOERLISMANDIGVDYL 265
 QY 263 EGQIFLSNGVVDTS--FFPPSDQSKVADLVKQHG-----IIVVLEVAKY-YDDPNLPII 313
 Db 266 EGFIVLNEQSLHSSSIAFPTN-----VDFNPDFGTKNNPKIYYCIEFAVHDYQNNKIN-V 319
 QY 314 SKVIDTLTKTLVLPFGFISMDHVAFFDLNRRHVEENKLSGLWELPHWPLNLYVPKSR 373
 Db 320 EQVVEVISRQMSHIAHLVSYVEVSFYDFLNRRHVEENKLSGLWELPHWPLNLYVPKSR 379
 QY 374 ILDFHNGVVKDILLKQKSA---SGLALLYPTNRNKNWNRMSAMPE--IDEDVYIIGLL 428
 Db 380 ISDF-----RDLMDISIPDNFEGILILYPLLRHKWDNTSVLPDSDGTDQVMYAVGIL 434
 QY 429 QSATPKDLPEVESVNEKIIRF-----CKDSGKIKQYLMHYTSKEDWIEHFGSKWDDFSK 483
 Db 435 RSANPDDGCSHHCLQELLRHRRLAGAAASGLGAKQYLAHPTPAGWRRHFGRRWERFAD 494
 QY 484 RKDLFDPKLLSPGQDIF 501
 Db 495 RKARFDPKLLSPGQDIF 512

RESULT 13
 Q9FUJ1 PRELIMINARY; PRT; 524 AA.
 ID Q9FUJ1
 AC Q9FUJ1;
 DT 01-MAR-2001 (TremBLrel. 16, Created)
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Cytochrome oxidase (FAD-linked oxidoreductase family).
 GN CKX5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bilyeu K.D., Laskey J.G., Riekhof W.R., VanVickle S., Morris R.O.,
 RT "A family of cytochrome oxidases from Arabidopsis thaliana."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Ronning C.M.,
 RA Smith Jr R.K., Arbogast T., Tallon L.J., Utterback T.R., VanAken S.E.,
 RA Feldblyum T.V., Yu C., Wortman J.R., White O., Fraser C.M.,
 RT "Arabidopsis thaliana chromosome 5 BAC F13M11 genomic sequence."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF303981; AAG30908.1; --
 DR EMBL; AC140977; AAO73882.1; --
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006094; Oxid_FAD_bind.
 DR Pfam; PF01565; FAD_binding_4; 1.
 DR SEQUENCE 524 AA; 57975 MW; 9ADB3BE97A7F063C CRC64;

Query Match 37.0%; Score 961; DB 10; Length 524;

Db 83 FGRENG---FAVVRGAAACSVDAQTSQSDGIVVDLSSLS-AVGEPAPSLVRVDGGARWRA 138
QY 134 VLKKTAEKGVSPVSWTDYLIHTVGGTSLNGGIGGVFRNGPLVSNVLELDVITCKGEMLT 193
Db 139 VLEATLPCGRVPLVVPDHLGLSVGGTSLVGGIGGTSHRYGVSADNVLELEVTTASGDLTT 198
QY 194 CSRQLNPELFYGVGLGQFGIITRARIVDHAPKRAKWFRLYSDFTTFTKDQERLISM 253
Db 199 CSPVRRPELFDVARGSLGRYGIITGATLALTGARSSARTYRLVYHDCAAFLADQQRLV-- 256
QY 254 ANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIYVLEVAKYYDDPNLP II 313
Db 257 -HERRFEHVEGHAHRSG---TS-----GWLFLVLEAMQSFDTPHEPDD 294
QY 314 SKVIDTLTKTLSYLPGFISMHDVAYFDFLNRVHVEENKLRSLGLWE-LPHPWLNLYVPKS 372
Db 295 TALLEGLTH-----HHVDTIETVSYRDFLGRVAPLEARQALGSWQHHPHRCNVLLP-- 347
QY 373 RILDFHNGVVVDILLKQKSA-----SGLALLYPTNRNKWDNRMSAMIPEIDE--DV 421
Db 348 -----GLEAEALITRTRTAGLTEEDIGPGGSVLLYPPIP-----TARLAA--PHVPKARDA 394
QY 422 IYIIGLLQSATPKDLPEV 439
Db 395 LTVVFGQLQRTAPPDQPEL 412

Search completed: April 5, 2004, 17:45:39
Job time : 49 secs

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OM protein - protein search, using sw model

Run on: April 5, 2004, 17:43:01 ; Search time 22 Seconds
(without alignments)
1175.664 Million cell updates/sec

Title: US-10-014-101-4
Perfect score: 2596
Sequence: 1 MANRLMLTILTVLMTKSS.....SKRKDLFPKLLSPGQDIF 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1141	44.0	534	3 US-09-124-541-1	Sequence 1, Appli
2	1141	44.0	534	4 US-09-663-326-1	Sequence 1, Appli
3	214.5	8.3	458	4 US-08-624-447-4	Sequence 4, Appli
4	193.5	7.5	495	3 US-09-217-490-2	Sequence 2, Appli
5	183.5	7.1	459	4 US-08-311-731A-47	Sequence 47, Appli
6	178	6.9	472	4 US-09-266-965-128	Sequence 128, App
7	177.5	6.8	610	4 US-09-630-983A-1	Sequence 1, Appli
8	175.5	6.8	600	4 US-09-423-468A-13	Sequence 13, Appli
9	175.5	6.8	600	4 US-09-630-983A-3	Sequence 3, Appli
10	174	6.7	468	4 US-09-328-352-6023	Sequence 6023, Ap
11	169	6.5	440	4 US-09-630-983A-9	Sequence 9, Appli
12	168.5	6.5	540	4 US-09-647-390-18	Sequence 18, Appli
13	166.5	6.4	592	4 US-09-423-468A-15	Sequence 15, Appli
14	166	6.4	1036	4 US-09-489-039A-10266	Sequence 10266, A
15	160	6.2	1019	4 US-09-543-681A-4447	Sequence 4447, Ap
16	159	6.1	535	4 US-09-589-733C-18	Sequence 18, Appli
17	155.5	6.0	538	4 US-09-647-390-16	Sequence 16, Appli
18	154	5.9	529	4 US-09-589-733C-17	Sequence 17, Appli
19	153.5	5.9	448	4 US-08-624-447-5	Sequence 5, Appli
20	151	5.8	529	4 US-09-589-733C-16	Sequence 16, Appli
21	149	5.7	538	4 US-09-589-733C-19	Sequence 19, Appli
22	146.5	5.6	514	4 US-09-266-965-114	Sequence 114, App
23	142.5	5.5	542	4 US-09-589-733C-2	Sequence 2, Appli
24	142.5	5.5	542	4 US-09-589-733C-20	Sequence 20, Appli
25	129.5	5.0	526	4 US-09-630-983A-5	Sequence 5, Appli
26	129.5	5.0	526	4 US-09-630-983A-7	Sequence 7, Appli
27	126.5	4.9	643	4 US-09-252-991A-23842	Sequence 23842, A

28	126	4.9	473	4 US-09-540-236-3656	Sequence 3656, Ap
29	116	4.5	529	4 US-09-252-991A-27777	Sequence 27777, A
30	116	4.5	725	3 US-08-425-843-2	Sequence 2, Appli
31	115	4.4	488	4 US-09-540-236-2681	Sequence 2681, Ap
32	113	4.4	529	4 US-09-433-248A-6	Sequence 6, Appli
33	113	4.4	614	4 US-09-328-352-4369	Sequence 4369, Ap
34	113	4.4	3169	4 US-09-453-702B-257	Sequence 257, App
35	110	4.2	422	4 US-09-634-238-227	Sequence 227, App
36	108	4.2	344	4 US-09-198-452A-857	Sequence 857, App
37	108	4.2	1012	1 US-08-219-262B-9	Sequence 9, Appli
38	108	4.2	1012	3 US-09-031-655-9	Sequence 9, Appli
39	105.5	4.1	527	4 US-09-252-991A-23709	Sequence 23709, A
40	105	4.0	715	3 US-08-425-843-7	Sequence 7, Appli
41	105	4.0	1012	1 US-08-219-262B-5	Sequence 5, Appli
42	105	4.0	1012	3 US-09-031-655-5	Sequence 5, Appli
43	104	4.0	816	4 US-09-328-352-6677	Sequence 6677, Ap
44	104	4.0	1012	1 US-08-219-262B-7	Sequence 7, Appli
45	104	4.0	1012	3 US-09-031-655-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-124-541-1
; Sequence 1, Application US/09124541A
; Patent No. 6229066
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/124,541A
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/054,268
; EARLIER FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-124-541-1

Query Match		44.0%;	Score 1141;	DB 3;	Length 534;
Best Local Similarity		47.0%;	Pred. No. 2.3e-105;		
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				Indels	28;
				Gaps	11;
Qy	30	SINLTSTDP	SIISAASHDFGNITTTVPGGVCPSSTADISRLLOYAANGKS--TFQVAA	87	
Db	42	ALDGLRTDSNATAAASTDFGNITSALPAALVPSSTGDLVALLS-AANSTPGWPYTIAF	100		
Qy	88	RGQHSNLNGQASVSGGVIWNMTCTD-----VVVSKDKKYADVAAGTLVDVLKKTAEK	141		
Db	101	RGHSLMGQAFAPGGVVVNMASLGDAAPPGINVSADGRYVDAGGEQVWIDVLRASLAR	160		
Qy	142	GVSPVSWTDYLIHTVGGTILSNGGIGGVFRNGPLVSNVLELDVITKGEMLTCSRQLNPE	201		
Db	161	GVAPRSWNDYLYLTVGGTILSNGAGISGQAFRHGPQISNVLEMDVITGHGEMVTCCKQLNAD	220		
Qy	202	LFYGVGLGGLGQFGIITRARIIVLDHAPKRAKWFRLYSDFTTFTKQERLISMANDIG---	258		
Db	221	LFDAVLGGLGQFGVITRARIATAVEPAPARARWVRFVYTDFAAFSADQERLTAPRPGGGAS	280		
Qy	259	---VDYLEGQIF---LSNGVVDTSTFFPPSDQSKVADLVKQHG--IIVVLEVAKYVDDPN	309		
Db	281	FGPMSYVEGVSFVNQSLATDLANTGFTTADADVARIVALAGERNATTVYSIEATLNYDNAT	340		
Qy	310	--LPIISKVIDTLTKTLSYLPQFISMDHVAVFDFLNRVHVVEENKLRSLGLWELPHWLN	367		
Db	341	AAAAVDQELASVLGTLVYEGFAFQRDVAYAAFLDRVHGEVALNKLGLWRVPHWLN	400		
Qy	368	YVPKSRILDFHNGVVKDILLKOKSASGLALLYPTNRNKWDMRMSAMPEIDEDVIYIIGL	427		

Db 401 FVPRSRIADFDGRVFKGI-LQGTDIVGLIYVPLNKSMMWDDGMSAATP--SEDFVYAVSL 457
QY 428 L-QSATPKDLPEVESVNEKIIREFCKDSGIKIKQYLMHYTSKEDWIEHFG-SKWDDFSKRK 485
Db 458 LFSSVAPNDLARLQEQNRRIILRFCDLAGIQYKTYLARHTDRSDWVRHFCAAKWNRFEVEMK 517
QY 486 DLFDPKKLLSPGQDIF 501
Db 518 NKYDPKRLSPGQDIF 533

RESULT 2
US-09-663-326-1
; Sequence 1, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: Morris Ph.D., Roy O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Zea mays
US-09-663-326-1

Query Match 44.0%; Score 1141; DB 4; Length 534;
Best Local Similarity 47.0%; Pred. No. 2.3e-105;
Matches 233; Conservative 83; Mismatches 152; Indels 28; Gaps 11;
QY 30 SLNLTSTDPSIIASAASHDFGNITTVTPGGVICPSTADISRLQLQYAAANGKS--TFQVAA 87
Db 42 ALDGKLRDTSNATAAASDFGNITSALPAAVLYPSTGDLVALLS-AANSTPGWPYTIAF 100
QY 88 RGQHSLSNGQASVSGGVIVNMTCTID-----VVVSKDKKYADVAAGTLWVDVLKKTAEK 141
Db 101 RGRGHSLSMGQAFAPGGVVVNMASLGDAAPPGINVSADGRYVDAGGEQVWIDVLRASLAR 160
QY 142 GVSPSWTDYLIHTVGGTSLNGGIGGOVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPE 201
Db 161 GVAPRSWNDYLYLTVGGTSLNAGISGQAFRHGQPOISNVLEMDVITGHGEMVTCCKQLNAD 220
QY 202 LFYGVGLGQFGIITRARIIVLDHAPKRAKWFRLMYSDFTTFTKQERLISMANDIG--- 258
Db 221 LFDVAVLGLGQFGVITRARIIVAEVAPARARWVRVYTDFAAFSADQERLTAPRPGGGGAS 280
QY 259 ---VDYLEGQIF---LSNGVVDTSPFPSPDQSKVADLVKQHG--IIYVLEVAKYDDPN 309
Db 281 FGPMXYVEGVSFVNQSLATDLANTGFTTDADVARIVALAGERNATTVYSIEATLNYDNAT 340
QY 310 --LPTISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLRSLGLWELPHWLN 367
Db 341 AAAAAVDQELASVLTGTLVYVEGFQFQRDVAYAAFLDRVHGEVALNKLGLMRVPHWLN 400
QY 368 YVPKSRILDFHNGVVKOILLKOKSASGLALLYPTNRNKNWNRMSAMIPEIDEDVIYIIGL 427
Db 401 FVPRSRIADFDGRVFKGI-LQGTDIVGLIYVPLNKSMMWDDGMSAATP--SEDFVYAVSL 457
QY 428 L-QSATPKDLPEVESVNEKIIREFCKDSGIKIKQYLMHYTSKEDWIEHFG-SKWDDFSKRK 485
Db 458 LFSSVAPNDLARLQEQNRRIILRFCDLAGIQYKTYLARHTDRSDWVRHFCAAKWNRFEVEMK 517
QY 486 DLFDPKKLLSPGQDIF 501
Db 518 NKYDPKRLSPGQDIF 533

RESULT 3

US-08-624-447-4
; Sequence 4, Application US/08624447A
; Patent No. 6524812
; GENERAL INFORMATION:
; APPLICANT: Sherman, David H.
; APPLICANT: August, Paul R.
; APPLICANT: Flickinger, Michael C.
; TITLE OF INVENTION: Genes encoding resistance to DNA
; TITLE OF INVENTION: bioreductive alkylating or cleaving agents and methods for
; TITLE OF INVENTION: identifying agents that inhibit resistance to DNA
; TITLE OF INVENTION: bioreductive alkylating and cleaving agents
; FILE REFERENCE: 600.458US1
; CURRENT APPLICATION NUMBER: US/08/624,447A
; CURRENT FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Arthrobacter oxidans
US-08-624-447-4

Query Match 8.3%; Score 214.5; DB 4; Length 458;
Best Local Similarity 24.5%; Pred. No. 1.3e-12;
Matches 69; Conservative 58; Mismatches 122; Indels 33; Gaps 10;
QY 35 LSTDPSSIISAASHDFGNITTVTPGGVI-CPS-----STADISRLQLQYAA-NGKSTFQVA 86
Db 9 LSIQGEVIYPQDSGFDANIMWDGRHLQRPISLIARCLSGADVAKSVRYACDNG--LEIS 65
QY 87 ARGQHSLSNGQASVSGGVIVNMTCTIDVVVSKDKKYADVAAGTLWVDVLKKTAEKGVSPV 146
Db 66 VRSQHNPNGYATNDGGIVLDLRLMNSIHIDTAGSRARIGGGVVISGDLVKEAAKFGLA 125
QY 147 SWTDYLIHTVG--GTLNCGGIGGQVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPELFY 204
Db 126 TG---MHPKVGFGLALNGGVGFLTPKYGLASDNLGATLVATGDIVYCSDDDERPELFW 182
QY 205 GVLGGLGQFGIITRARIIVLDHAPKRAKWFRLMYSDFTTFTKQERLISMANDIGVDYLEG 264
Db 183 AVRGAGPNFGVTEVEVQLYELP-----RKMLAGFITWAPSVSELAGLITSL-LDAL-- 233
QY 265 QIFLSNGVVD---TSFFPSPDQSKVADLVKQHGIIYVLEVAK 303
Db 234 ----NEMADHIYPSVFGVDENRAPSVTVVCVGHGLGLDIAE 270

RESULT 4
US-09-217-490-2
; Sequence 2, Application US/09217490
; Patent No. 6165761
; GENERAL INFORMATION:
; APPLICANT: Schneider, Palle
; APPLICANT: Christensen, Soren
; APPLICANT: Dybdal, Lone
; APPLICANT: Fuglsang, Claus Crone
; APPLICANT: Xu, Feng
; APPLICANT: Golightly, Elizabeth
; TITLE OF INVENTION: Carbohydrate Oxidase And use Thereof In
; FILE REFERENCE: 5421.200-US
; CURRENT APPLICATION NUMBER: US/09/217,490
; CURRENT FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: PA 1997 01505
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: PA 1998 00763
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/068,717
; EARLIER FILING DATE: 1997-12-23

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; EARLIER APPLICATION NUMBER: 60/088/725
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Microdochium nivale
US-09-217-490-2

Query Match          7.5%; Score 193.5; DB 3; Length 495;
Best Local Similarity 20.4%; Pred.No. 1.9e-10;
Matches 110; Conservative 82; Mismatches 225; Indels 121; Gaps 20;

QY 7 MITLITVLMITK-----SSNGIKIDLPKSLNLTSTDPSTIISAASHDFGNITVTPGG 59
Db 11 LITASADALVTRGAIEACLSAAGVPIDIPGTADYERDVEP-----FNIRLPYIPTA 61

QY 60 VICPSSSTADISRLLOAYANGKSTFFQVARGQGHSLN--GQASVSGGVIVNMTCTITDVVVS 117
Db 62 IAQTOTTAHTQSAVQCAK--KLNKVSAGSGGHSYASFGFGGNGHLMVQLDRMIDVISY 119

QY 118 KDKK-YADVAAG-----TLWVDVLKKTAEKGVSPVSWTDYHLHITVGGTSLNNGGIGGQV 169
Db 120 NDKTGIAHVEFGARLGHLATVLDNKYGRAISHGTCP-----GVGISGHFAHGGFGFESS 172

QY 170 FRNGPLVSNVLELDVITGKGEMLTCSRQLNPFLFYGLVGLGQFGIITRARIIVLDHAPKR 229
Db 173 HMGHLAVDSVVGTVVLADGRIVEASATENADLFWGIKAGSNFGLVAVWKLATFPAPKV 232

QY 230 AKWF--RMLYSDFTTFTKQERLISMANDIG---VDYLEGQIFLSNGVVDTTSFFPPSDQS 284
Db 233 LTRFGVTLNWKNTSALKGIEAVEDYARVAPREVNFRIGDYGAGNPGIEGLYYGTPEQW 292

QY 285 KVADLVKQHGIIVVLEVAKYDDPNLPILSKVIDTL-----TKTLSYLPGFISMHDV 336
Db 293 RAA-----FOPLDITLPAGYVNVNPTSLNWIESVLSYSNF 327

QY 337 AYDFLNRVHVEENKRLSLGLWELPHPLNLYVP-----KSRI-----LDFHNGVVK 383
Db 328 DHVDFITPQPVENFYAKSLTLKSIKGDVAKNFVDYDFVSNKVKDRFWFYQLDVHGGKNS 387

QY 384 DILLKQKSASGLALLYPTNRNKW-----DNRMSAMPEIDEDVIYIIGLLQSATPKD 435
Db 388 QV-----TKVTNAETAYPHRDKLWLIQFYDRYDNNQT--YPE--TSFKELDGWVNSVT-KA 438

QY 436 LPEVE---SVNEKIIIFCKDSGIKIKQYLMHYTSKEDWIEHFGSKWDDFSKRKOLFDP 490
Db 439 LPKSDWGMVINYADPRMDRDYATKV-----YYGENLARLQKLKAKFDP 481

RESULT 5
US-08-311-731A-47
; Sequence 47, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-47

Query Match          7.1%; Score 183.5; DB 4; Length 459;
Best Local Similarity 30.4%; Pred.No. 1.7e-09;
Matches 55; Conservative 29; Mismatches 88; Indels 9; Gaps 3;

QY 111 ITDVV-VSKDKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYHLHITVGGTSLNNGGIGGQV 169
Db 58 LTGVIGIDTEARTADVAGMCTYEDLVAATLPYGLLPLVVPQLKTTITLGGAVTGLGIESAS 117

QY 170 FRNGPLVSNVLELDVITGKGEMLTCSRQLNPFLFYGLVGLGQFGIITRARIIVLDHAPKR 229
Db 118 FRNGLPHEVLEMDILTGAHELLTVSANQHGDLYRAFNPNSYGTGLYSTFRISLEPVTFF 177

QY 230 AKWFRMLYSDFTTFTKQERLISMANDIG---VDYLEGQIFLSN-----GVVDTTSFFPPS 281
Db 178 VALRHIRFHLLTEMVTAMENIIDTGGHDGVPVDYLDGVVFSANESYLCIGKRTTTPGPVS 237

282 D 282
238 D 238

RESULT 6
US-09-266-965-128
; Sequence 128, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 128
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Streptomyces lavendulae
US-09-266-965-128

Query Match          6.9%; Score 178; DB 4; Length 472;
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Db 139 QVVALTLMTADGEVLECSERNADVFOAARVHLGCLGIILTVTLQCVQFQLQETSPFST 198
QY 222 ---VLDHAP---KRAKWERMLYSDFE-----TFTKDQERLISMANDIGVDYLEGOIFLSN 270
Db 199 LKEVDNLDLSHLKSEYFRFLWFPHTENVSIYQDHTNKAPSSASGNWFWDYAIG----- 252
QY 271 GVVDTSFFPPSDQSKVADLVKQHGIIVYLEVAKYDDPNLPIISKVIDTLTKTLSYLP-- 328
Db 253 -----FYLLFEF-----LLWTSTYLPCL 269
QY 329 -GFIS-----MHDVAYDFELNRVHVEENKLSLGLWELP-HPWLNLYV 369
Db 270 VGWINRFFFWMLFNCKESSNLSHKIFTYECPKQHVQD-----WAIPREKTKEALL 321
QY 370 PKSRILDFHNGVVKDILLKQKSASGLALLYPTRNKNWDRMSAMIPEDIDEDVIYIIGLLQ 429
Db 322 ELKAMLEAHPKVVAHYPEVFRTRGDDIL-----LSPCFQORDSCYMNIIY 367
QY 430 SATPKDLPESVNEKIIRFCCKDSGKIKIQYLMHYTSKEDWIEHFGSKWDDFSKRRKDLF- 488
Db 368 RPYGKDVPRL-----DYWLAYETIMKKFGGRPHWAKAHNCTQKDFEEMYPTEH 415
QY 489 ---DPKKLLSP 496
Db 416 KFCDIREKLDLP 426

RESULT 12
US-09-647-390-18
; Sequence 18, Application US/09647390
; Patent No. 6465636
; GENERAL INFORMATION:
; APPLICANT: Stuiver, Maarten
; APPLICANT: Custers, Jerome
; APPLICANT: Simons, Lambertus
; TITLE OF INVENTION: Pathogen-Inducible Promoter
; FILE REFERENCE: MOG 57707/UST
; CURRENT APPLICATION NUMBER: US/09/647,390
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: EP 98201024.1
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: PCT/EP99/02178
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Lactuca sativa
US-09-647-390-18

Query Match 6.5%; Score 168.5; DB 4; Length 540;
Best Local Similarity 23.5%; Pred. No. 7.1e-08;
Matches 81; Conservative 50; Mismatches 124; Indels 89; Gaps 14;
QY 28 PKSLNLTSLDPSIISAASHDFGNITVTTPGGVICPSSTADISRLLOQYAANGKSTFQVAA 87
Db 81 PKPILIIITLHPHSIQAA-----VVC-----AKTHRLMLKTRSG----- 114
QY 88 RGQGHSLNGQASVSGG---VIVNMTCTDWWVSKOKKYADVAAGTLWVDVLKKTAEK-- 141
Db 115 ---GHDYEGLSYVTNSNQPFVVDMFNLSINVSIEDETAWVQAGATLGEVYVRIAEKSN 171
QY 142 -----GVSPVSWTDYLHITVGGTSLNGGIGGQVFRNGPLVSNVLELDVITKGEMLTCS 195
Db 172 SHAFPAVGVCP-----VGVGHFSGGGYGNLMGKYGSLVDNIYDAQLIDVNGKLLN-R 223
QY 196 RQLNPFLFYGLGLG-QFGIITRARIIVLDHAPKRAKWFRLMYSDFTTFTKQOERLISMA 254
Db 224 KSMGEDLFWAITGGGVSGFVWVAYKIKLVRVPTTIVFNVQRTSEQNLSIAHRWIQVA 283
QY 255 NDIGVDYLEGOIFLS---NGVVDTS-----FFP-----PSDQSKV 286

Db 284 -----DKJDNDFELRMTFNVINNTNGEKTIRGLFPTLYLGNSTALVALLNKDFPELGVFI 338
QY 287 ADLVKQHGIIVYLEVAKYDDPNLPIISKVIDTLTKTLSYLPGF 330
Db 339 SDCIEMSWIESVL-----FY--TNFPICGPTTALLSRTQPRLNPF 376
RESULT 13
US-09-423-468A-15
; Sequence 15, Application US/09423468A
; Patent No. 6469149
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
; APPLICANT: Mark William Davey
; APPLICANT: Jens Ostergaard
; APPLICANT: Marc Charles Ernest Van Montagu
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLES.001APC
; CURRENT APPLICATION NUMBER: US/09/423,468A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: NL 1006000
; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-423-468A-15

Query Match 6.4%; Score 166.5; DB 4; Length 592;
Best Local Similarity 19.9%; Pred. No. 1.3e-07;
Matches 94; Conservative 84; Mismatches 198; Indels 97; Gaps 19;
QY 63 PSSTADISRLLOQYAANGKSTFQVAAARGQHSNGQASVSGGVIVNMTCTIDVV-VSKDKK 121
Db 129 PENLADLEALVKESHEKK--LRIRPVGSLSPNG-IGLSRSGMNLALMDKVLVDKEKK 185
QY 122 YADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSL-----NGGIGGQVFRNGPLV 176
Db 186 RVTVQAGIRVQQLVDAIKDYGLTLQNFASIREQQIGGIQVFFVYVQVGAHGTGARLPPID 245
QY 177 SNVLELDVITKGEMLTCSRQINPELFGVLGGLGQFGIITRARIIVLDHAPKRAKWFRLM 236
Db 246 EQVISMKLVTPAKGTIELSREKDPFLFHLARCGGLGVV--AEVTLQCVARHELVEHTY 303
QY 237 YSDFTTFTKQERLISMAND----IGVDYLEGOIFLSNGVVDTSFFPPSDQSK----- 285
Db 304 VSNLQEIKNHKKLLS-ANKHVXYLYPYTDTVVVVTCNPVSKWSGPPKDKPKYTTDEAV 362
QY 286 --VADLVKQHGIY--VLEVAKYDDPNLPIISKVIDTLTKTLSYLPGFISMHD-VAYFD 340
Db 363 QHVRDLVRESIVKYRRVQDSGKSPDSSEPDIQEL-----SFTELRDKLLALD 410
QY 341 FLNRVHVEENKLSLGLWELP-----HPWLN-----LYVPKSR 374
Db 411 PLNDVHVGKVNQAEAEFWKKSEGYRVGWSDEILGDCGQGVVSESCFPAGTLANPSMKD 470
QY 375 LDFHNGVVKDILLKQKSASGLALLYPTRNKNWDRMSAMIP---EIDEDVIY--IIGLLQ 429
Db 471 LEYIEELKK-LIEKEAIPAPAPI---EQRWTARSKSPISPAFSTSEDDIFSWVVGIIIM 524
QY 430 SATPKDLPESVNEKIIRFCCKDSGKIKIQYLMHYTSKEDWIEHFGSKWDDFS 482
Db 525 YLPTADPRQRKDITDEFFHY-----RHLTQKQ-----LWDQFS 557

RESULT 14
US-09-489-039A-10266
; Sequence 10266, Application US/09489039A
; Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10266
LENGTH: 1036
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10266

Query Match 6.4%; Score 166; DB 4; Length 1036;
Best Local Similarity 18.8%; Pred. No. 3.8e-07;
Matches 114; Conservative 102; Mismatches 200; Indels 190; Gaps 27;

QY 4 LRLMITLITVLMITKSSNGIKIDLPKSL--NLTLSTDPSSIISAASHDFGNITVTTPGGVI 61
Db 30 VQLVLNFLQVL-----EQQFTGDTATSYADRLTMATDNSVYQ-----LLPDAVI 74

QY 62 CPSSTADISRLQLQYAANGK-STFQVAARGQGHSLNGQASVSGGVIVNMTCTID--VVVSK 118
Db 75 FPRSTADVALLARVAAPRFSKLIPTPRGGGTGTNGQA-LNGGIIVDMSRYMNRRIIEINP 133

QY 119 DKKYADVAAGTLWVDVLKKTAEKGVSPVSW-----TDYLHITVGGTSLNSGGIGGVQVFN 172
Db 134 EEGWVRVEAG-----VIKQNLNQLFKPYGFFFAPELSTSNRATLGGMINTDASGGQSLVY 188

QY 173 GPLVSNVLELDVITKGEML-----TCSRQ----- 197
Db 189 GKTS DHVLGLRAVLGMGGDILDQTQAVPVALAETLGNTPSTVGRIVNTVYQRCQAQRDLIID 248

QY 198 ----LNP-----ELFYGVGLGGLQFGIITRARIIVLDHAPKRAKWF 235
Db 249 KFPKLNRLFTGYDLRHVFNDSEFDTLRLTGTSEGLAFITEARLDITRLPKVRRLVNV 308

QY 236 LYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQ--- 292
Db 309 KYDSFDSALRNAPFMVE-AKALSVEITVD-----SKVLNLAREDIV 347

QY 293 -HGI-----IYVLEVAKYDDPNLPIISKVIDTLTKTSLYLP-----GFI 332
Db 348 WSHVSELITDVPDKEMGLNIVEFAGD-DAALIDQQVTTLCORLDELMAASEAGVIGQV 406

QY 333 MHDVAYDFLNRVHVEENKLSLGLW-----ELPHPWL-NLYVPKSRILDFHNGVVKDI 385
Db 407 CHDL---EGVERIYAMRKK--AVGLLGNAKGAKEPIFFAEDTCVPPPEHLADY---IVEFR 458

QY 386 LLKOKSASGLALLYPTNRNKNWNRMSAMIPEIDEDVIYIIGLLQSATPKDLPEVESVNEK 445
Db 459 AL--LD SHGLSY-----GMFGHVDAGVLHVRPALDMCDPQQEILMKQISDE 502

QY 446 IIRFKD SGIKIKQYLMHYTSKEDWIEH-----FG-SKWDDF SKRKDLFDPKK 492
Db 503 VVALTAKYGGLL-----WGEHGKGFRAEYSPAFFGETLYAELRKIKAVFDPDN 550

QY 493 LLSPGQ 498
Db 551 RLNPGK 556

RESULT 15
US-09-543-681A-4447
Sequence 4447, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4447
LENGTH: 1019
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4447

Query Match 6.2%; Score 160; DB 4; Length 1019;
Best Local Similarity 19.2%; Pred. No. 1.5e-06;
Matches 114; Conservative 99; Mismatches 208; Indels 172; Gaps 27;

QY 10 LITVLMITKSSNGIKIDLPKSL--NLTLSTDPSSIISAASHDFGNITVTTPGGVICPSSTA 67
Db 15 LTTEFLNLTQRNGFTGDISSTYADRLTMATDNSIQ-----LLPQAVIFPRSTA 63

QY 68 DISRLQLQYAANGK-STFQVAARGQGHSLNGQASVSGGVIVNMTCTID--VVVSKDKKYAD 124
Db 64 DVTIVARLVDEPRFHSLSLTPRGGGTGTNGQA-LTEGIVVDLSRYMKRIIEINPEQRWVK 122

QY 125 VAAGTLWVDVLKKTAEKGVSPVSW-----TDYLHITVGGTSLN--GGIGGVQVFRNGPLV 176
Db 123 VEAG-----VIKDELNLFLKPYGFFFAPELSTSNRATLGGMINTDASGGQSMVY--GKTS 175

QY 177 SNVLELDVITKGEML-----TCSRQLNPELF-- 203
Db 176 DHVLGVRAVLGGLLETRAMDSALAEITAKEDSAVGRIYQTVLSRCKAQRQLILEKFPK 235

QY 204 -----YG-----VLGGLGQFGIITRARIIVLDHAPKRAKWF 239
Db 236 LNRFLTGYDLRHVFSDDMKHFDLRLTGTSEGLAFITEATLDTIPKORSLVNVKYDS 295

QY 240 FTTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQ---HGI 295
Db 296 FDSALRNAPFLVK-AKALSVEITVD-----SKVLNLAREDIVVWHSV 334

QY 296 -----IYVLEVAKYDDPNLPIISKVID---TLTKTSLYLPGFISMHDVA-YED 340
Db 335 NALITDVPDKMQGLNIVEFAGDDKTLIASQVEDLCQRLDKLMNNGEGGVIGVQVCDNLA 394

QY 341 FLNRVHVEENKLSRLGL-----WELPHPWL-NLYVPKSRILDFHNGVVKDILLKQKSAS 393
Db 395 DINRIYAMRKK--AVGLLGNAKGHAKPIPFVEDTCVPPPEHLADY-----ITE 439

QY 394 GLALL--YPTNRNKNWNRMSAMIPEIDEDVIYIIGLLQSATPKDLPEVESVNEKLIIRFCK 451
Db 440 FRALLDSYQLN-----YGMFGHVDAGVLHVRPALDMCDPQQEQLMKTISDEIVALTA 491

QY 452 DSGIKI-----KQYLMHYTSKEDWIEHFG-SKWDDF SKRKDLFDPKKLLSPGQ 498
Db 492 KYGGLLWGEHGKGFRAQYSP-----EFFGETLYHELRLQIKTVFDPNRNRLNPGK 539

Search completed: April 5, 2004, 17:46:46
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: April 5, 2004, 17:45:47 ; Search time 46 Seconds
(without alignments)
2860.031 Million cell updates/sec

Title: US-10-014-101-4
Perfect score: 2596
Sequence: 1 MANLRMLTILITVLMITKSS.....SKRKDLFPDKKLLSPGQDIF 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2596	100.0	501	12	US-10-311-453-4
2	2596	100.0	501	14	US-10-014-101-4
3	1822	70.2	524	12	US-10-311-453-8
4	1822	70.2	524	14	US-10-014-101-8
5	1292	49.8	523	12	US-10-311-453-6
6	1292	49.8	523	14	US-10-014-101-6
7	1184	45.6	536	12	US-10-311-453-10
8	1184	45.6	536	14	US-10-014-101-10
9	1184	45.6	539	12	US-10-311-453-35
10	1184	45.6	539	14	US-10-014-101-35
11	1126.5	43.4	611	9	US-09-829-549A-48
12	1056.5	40.7	575	12	US-10-311-453-2
13	1056.5	40.7	575	14	US-10-014-101-2
14	993	38.3	504	12	US-10-311-453-12
15	993	38.3	504	14	US-10-014-101-12

16	950.5	36.6	407	12	US-10-424-599-152644	Sequence 152644,
17	939	36.2	513	12	US-10-424-599-220961	Sequence 220961,
18	805.5	31.0	392	12	US-10-425-114-39823	Sequence 39823, A
19	745	28.7	324	12	US-10-424-599-144567	Sequence 144567, A
20	745	28.7	324	12	US-10-425-114-42126	Sequence 42126, A
21	661.5	25.5	292	12	US-10-425-114-40061	Sequence 40061, A
22	661.5	25.5	299	12	US-10-424-599-162425	Sequence 162425,
23	620.5	23.9	334	12	US-10-424-599-155687	Sequence 155687,
24	612	23.6	290	12	US-10-425-114-39759	Sequence 39759, A
25	587	22.6	290	12	US-10-424-599-144566	Sequence 144566,
26	457	17.6	487	14	US-10-166-087-14	Sequence 14, Appl
27	440.5	17.0	230	12	US-10-424-599-255266	Sequence 255266,
28	421	16.2	173	12	US-10-425-114-52875	Sequence 52875, A
29	401.5	15.5	214	12	US-10-424-599-200943	Sequence 200943,
30	379	14.6	276	12	US-10-425-114-46334	Sequence 46334, A
31	353	13.6	143	12	US-10-424-599-205473	Sequence 205473,
32	336	12.9	229	12	US-10-425-114-39997	Sequence 39997, A
33	326.5	12.6	203	12	US-10-424-599-148081	Sequence 148081,
34	324	12.5	187	12	US-10-424-599-220960	Sequence 220960,
35	314.5	12.1	202	12	US-10-424-599-212362	Sequence 212362,
36	293	11.3	99	12	US-10-424-599-204492	Sequence 204492,
37	293	11.3	99	12	US-10-425-114-56907	Sequence 56907, A
38	235	9.1	118	12	US-10-424-599-256584	Sequence 256584,
39	226.5	8.7	515	9	US-09-738-626-4135	Sequence 4135, Ap
40	214	8.2	88	12	US-10-424-599-148123	Sequence 148123,
41	214	8.2	296	12	US-10-425-114-42202	Sequence 42202, A
42	206	7.9	122	12	US-10-424-599-220958	Sequence 220958,
43	193.5	7.5	495	14	US-10-314-190-2	Sequence 2, Appli
44	185	7.1	439	14	US-10-156-761-9946	Sequence 9946, Ap
45	179.5	6.9	461	15	US-10-369-493-11223	Sequence 11223, A

ALIGNMENTS

RESULT 1
US-10-311-453-4
; Sequence 4, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-4

Query Match	100.0%;	Score 2596;	DB 12;	Length 501;
Best Local Similarity	100.0%;	Pred. No. 9.6e-233;		
Matches 501;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MANLRMLTILITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTGGV	60	
Db	1	MANLRMLTILITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTGGV	60	
QY	61	ICPSSSTADISRLLOQAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCTIDVWVSKDK	120	
Db	61	ICPSSSTADISRLLOQAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCTIDVWVSKDK	120	

QY 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLVSNVL 180
Db 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLVSNVL 180
QY 181 ELDVITKGEMLTCSRQNLPELFYGVGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF 240
Db 181 ELDVITKGEMLTCSRQNLPELFYGVGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF 240
QY 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSPFPSPDQSKVADLVKQHGIIYVLE 300
Db 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSPFPSPDQSKVADLVKQHGIIYVLE 300
QY 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLSLGLWEL 360
Db 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLSLGLWEL 360
QY 361 PHPWNLVYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDMRMSAMIPEIDED 420
Db 361 PHPWNLVYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDMRMSAMIPEIDED 420
QY 421 VIYIIGLLQSATPKOLPEVESVNEKIIREFCKDSGIIKQIYLMHYTSKEDWIEHFGSKWDD 480
Db 421 VIYIIGLLQSATPKOLPEVESVNEKIIREFCKDSGIIKQIYLMHYTSKEDWIEHFGSKWDD 480
QY 481 FSKRKDLFDPKLLSPGQDIF 501
Db 481 FSKRKDLFDPKLLSPGQDIF 501

RESULT 2

US-10-014-101-4
; Sequence 4, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-4

Query Match 100.0%; Score 2596; DB 14; Length 501;
Best Local Similarity 100.0%; Pred. No. 9.6e-233;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLRMTLITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTTPGGV 60
Db 1 MANLRMTLITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTTPGGV 60
QY 61 ICPSSSTADISRLLQYAANGKSTFQVAARGQGHSLNGQASVSGGIVNMTCTIDVVVSKDK 120
Db 61 ICPSSSTADISRLLQYAANGKSTFQVAARGQGHSLNGQASVSGGIVNMTCTIDVVVSKDK 120
QY 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLVSNVL 180
Db 121 KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGGVFRNGPLVSNVL 180

QY 181 ELDVITKGEMLTCSRQNLPELFYGVGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF 240
Db 181 ELDVITKGEMLTCSRQNLPELFYGVGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF 240
QY 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSPFPSPDQSKVADLVKQHGIIYVLE 300
Db 241 TTFTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSPFPSPDQSKVADLVKQHGIIYVLE 300
QY 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLSLGLWEL 360
Db 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDFLNRVHVEENKLSLGLWEL 360
QY 361 PHPWNLVYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDMRMSAMIPEIDED 420
Db 361 PHPWNLVYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDMRMSAMIPEIDED 420
QY 421 VIYIIGLLQSATPKOLPEVESVNEKIIREFCKDSGIIKQIYLMHYTSKEDWIEHFGSKWDD 480
Db 421 VIYIIGLLQSATPKOLPEVESVNEKIIREFCKDSGIIKQIYLMHYTSKEDWIEHFGSKWDD 480
QY 481 FSKRKDLFDPKLLSPGQDIF 501
Db 481 FSKRKDLFDPKLLSPGQDIF 501

RESULT 3

US-10-311-453-8
; Sequence 8, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-8

Query Match 70.2%; Score 1822; DB 12; Length 524;
Best Local Similarity 66.7%; Pred. No. 1.3e-160;
Matches 345; Conservative 69; Mismatches 79; Indels 24; Gaps 5;

QY 7 MITLITVLM-----ITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTTPGGVI 61
Db 9 LITLITLFIISLTPTLIKSDGIDVPLPISLNLTLVTDPPSISAASHDFGNITDENPGAVL 68
QY 62 CPSSTADISRLLQYAANG-----KSTFQVAARGQGHSLNGQASVSGGIVNMTCI 111
Db 69 CPSSTTEVARLLRFPANGGFSYNGKSTSPASTFKVAARGQGHSLRGOASAPGGVVNMTCL 128
QY 112 -----TDVVVSKDKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGI 165
Db 129 AMAAKPAAVVISADGTYADVAAGTWWVDVLKAAVDRGVSPVTWTDLYLSVGGTSLSNAGI 188
QY 166 GGQVFRNGPLVSNVLELDVITGKEMLTCSRQLNPPELFYVGLGGLGQFGIITRARIIVLDH 225
Db 189 GGQTFRHGQIISNVHELVDVITGKEMMTCSKLNPELFYVGLGGLGQFGIITRARIIVLDH 248
QY 226 APKRAKWFRLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSPFPSPDQSK 285

Db 249 APTRVKWSRILYSDFSAFKRDQERLISMTNDLGVDFLEGQLMMSGFVDTSPFFLSDQTR 308
QY 286 VADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKTLSYLPGFISMHDVAYFDFLNRV 345
Db 309 VASLVNDHRIIYVLEVAKYVDRDTLPIIDQVIDTSLRSLGFAPGFMFVQDVPYFDFLNRV 368
QY 346 HVEENKLRSLGLWELPHPWLNLYVPKSRILDFHNGVVVDKILLKQKSASGLALLYPTNRNK 405
Db 369 RNEEDKLRSLGLWEVPHPWLNIFVPGSRIQDFHDGVINGLLNQTSTSGVTLFYPTNRNK 428
QY 406 WDNRMASAMPEIDEDVYIIGLLQSA-TPKDLPEVESVNEKIIRFCKDSGIIKIQYLMHY 464
Db 429 WNNRMSTMTTP--DEDVFYVIGLLQSAGGSQNWQOLENLNDKVIQFCENSIGIKIKEYLMHY 486
QY 465 TSKEDWIEHFGSKWDDFSKRKDLFDPKKLLSPGQDIF 501
Db 487 TRKEDWVKHFGPKWDDFLRKKIMFDPKRLLLSPGQDIF 523

RESULT 4
US-10-014-101-8
; Sequence 8, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-8

Query Match 70.2%; Score 1822; DB 14; Length 524;
Best Local Similarity 66.7%; Pred. No. 1.3e-160;
Matches 345; Conservative 69; Mismatches 79; Indels 24; Gaps 5;

QY 7 MITLITVLM-----ITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTTPGGVI 61
Db 9 LITLITLFIISLTPTLIKSDGIDVFLPISLNLTLVTDPPSISAASHDFGNITDENPGAVL 68
QY 62 CPSSTADISRLLQYAANG-----KSTFQVAARGQGHSLNGQASVSGGVIVNMTCI 111
Db 69 CPSSTTEVARLLRFANGGFSYNGKSGTSPASTFKVAARGQGHSLRGQASAPGGVVNMTCL 128
QY 112 -----TDVVVSKOKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGI 165
Db 129 AMAAKPAAVVISADGTYADVAAGTMWVDVLKAAVDRGVSPVTWTDYLYLSVGGTSLNAGI 188
QY 166 GGOVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPELFGVLGGLGQFGIITRARIIVLDH 225
Db 189 GGOFRHGPPQISNVHELVDITGKGEMLTCSRQLNPELFGVLGGLGQFGIITRARIIVLDH 248
QY 226 APKRAKWFRLMYSDFTTFTTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSFPFSDQSK 285
Db 249 APTRVKWSRILYSDFSFAKRDQERLISMTNDLGVDFLEGQLMMSGFVDTSPFFLSDQTR 308
QY 286 VADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKTLSYLPGFISMHDVAYFDFLNRV 345

Db 309 VASLVNDHRIIYVLEVAKYVDRDTLPIIDQVIDTSLRSLGFAPGFMFVQDVPYFDFLNRV 368
QY 346 HVEENKLRSLGLWELPHPWLNLYVPKSRILDFHNGVVVDKILLKQKSASGLALLYPTNRNK 405
Db 369 RNEEDKLRSLGLWEVPHPWLNIFVPGSRIQDFHDGVINGLLNQTSTSGVTLFYPTNRNK 428
QY 406 WDNRMASAMPEIDEDVYIIGLLQSA-TPKDLPEVESVNEKIIRFCKDSGIIKIQYLMHY 464
Db 429 WNNRMSTMTTP--DEDVFYVIGLLQSAGGSQNWQOLENLNDKVIQFCENSIGIKIKEYLMHY 486
QY 465 TSKEDWIEHFGSKWDDFSKRKDLFDPKKLLSPGQDIF 501
Db 487 TRKEDWVKHFGPKWDDFLRKKIMFDPKRLLLSPGQDIF 523

RESULT 5
US-10-311-453-6
; Sequence 6, Application US/103111453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-6

Query Match 49.8%; Score 1292; DB 12; Length 523;
Best Local Similarity 48.5%; Pred. No. 3.2e-111;
Matches 251; Conservative 106; Mismatches 138; Indels 22; Gaps 6;

QY 3 NLRIMITLIT--VLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGN 51
Db 5 NLRSQVRLIAITVITLSTPITNTSPQPMNLSHNEFAGKLTSSSSSVESAATDFGH 64
QY 52 ITTVPGGVICPSSTADISRLLQYAANGKSTFQVAARGQGHSLNGQASVSGGVIVNMTCI 111
Db 65 VTKIFPSAVLIPSSVEDITDLIKLSFDSQLSPFLAARGHSHRGQASAKDGVVNNRSM 124
QY 112 TD---VVVSKOKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLHITVGGTSLNGGIGG 167
Db 125 VNRDRGIKVSRTCLYVDVDAAWLWIEVLNKTLELGLTPVSWTDYLYLTVGGTSLNGGISG 184
QY 168 QVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPELFGVLGGLGQFGIITRARIIVLDHAP 227
Db 185 QTFRYGQITNVLEMDVITGGEIATCSKDMNSDLFFAFLGGLGQFGIITRARIIVLEVAP 244
QY 228 KRAKWFRLMYSDFTTFTTKDQERLISMANDIGVDYLEGQIFLSNGVVD--TSFFPPSDQS 284
Db 245 KRAKWLFLYIDFSEFTRDQERVISKTD--GVDFLEGSIMVDHGPPDNWRSTYPPSDHL 302
QY 285 KVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKTLSYLPGFISMHDVAYFDFLNR 344
Db 303 RIASMVKRHRVIYCLEVVKYDETSTQYTVNEEMEELSDSLNVHRGFMYEKDVITYMDFLNR 362
QY 345 VHVEENKLRSLGLWELPHPWLNLYVPKSRILDFHNGVVVDKILLKQKSASGLALLYPTNRN 404
Db 363 VRTGELNLKSKGQWDVPHPWLNLFVPKTQISKFDDGVFKGIILRNNTTSGPVLVYPMNRN 422

```

405 KWDNRMSAMPEIDEDVYIIGLLQSATPKDLPEVESVNEKIIRFCXSGIKIQYLMHY 464
423 KWNDRMSAAIPE--EDVFAVGFRLRSAGFDNWEAFDQENMEILKFCEDANMGVIQYLPYH 480
465 TSXEDWIEHFGSKWDDFSKRXDLDFDPKLLSPGQDIF 501
481 SSQEGWVRHFGRWNIFVERKYKYDPKMLSPGQNIF 517

RESULT 6
US-10-014-101-6
; Sequence 6, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-6

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QY      465   TSKEDWIEHFGSKWDDFSRRKDLFDPKLLSPGQDIF 501
        :| | | :| | | :| | | :| | | :| | | :| | |
DB      481   SSQEGWVRHFGRWNIFVERKYKYDPKMILSPGQNIF 517

RESULT 7
US-10-311-453-10
; Sequence 10, Application US/103111453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-10

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RESULT 8
US-10-014-101-10
; Sequence 10, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:


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; LENGTH: 539
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-35

Query Match      45.6%; Score 1184; DB 14; Length 539;
Best Local Similarity 48.8%; Pred. No. 3.9e-101;
Matches 233; Conservative 84; Mismatches 142; Indels 18; Gaps 7;

QY 39 PSIIASAASHDFGNI-TTVPGGVICPSSSTADISRLLOXAANGKSTFOVAARGQHSLNGQ 97
Db 47 PSDLASVSSDFGMLKSPPEPLAVLHPSSAEDVARLVRTAYGSATAPFVSARGHGSINGQ 106
QY 98 ASVS-GGVIVNM-----TCITDVVWSKDKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYL 152
Db 107 AAAGRGVVVEVMNHGVTGTPKPLVRPDEMYVDVWGGELWVDVLKKTLEHGLAPKSWTDYL 166
QY 153 HITVGGTSLNGGIGGVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPFLFYGLGLGQ 212
Db 167 YLTVGGTSLNAGISGQAFHHGPOISNVLELDVVTGKGEVMRCSEEEENTLFGHVLGLGQ 226
QY 213 FGIITRARIIVLDHAPKRAKWFRLMYSDFTTFTTKDQERLISMANDIGVDYLEGQIFLSNGV 272
Db 227 FGIITRARIISLEPAPQVRWIRVLYSSFKVFIEDQEYLISMHGQLKFDYVEGFVIVDEGL 286
QY 273 VD---TSFPFPPSDQSKVADLVKQHGIIYVLEVAKYVDDPNLPIISKVIDTLTKTSLYLP 329
Db 287 VNNWRSSFFSPNPVPISSVSSNGSVLYCLEITKNYHSDSEIVDQVEILMKLNFIPT 346
QY 330 FISMHDVAYDFLNRVHVEENKRLSLGLWELPHEWNLVYVPKSRILDFHNGVVKDILLKQ 389
Db 347 SVFTTDLQYVDFLDRVHKAELKRLSKNLWEVPHWNLVFPKSRISDFDKGVFKGIL--G 404
QY 390 KSASGLALLYPTNRNKNWDRMSAMIPEIDEDVYIIGLLQSA-----TPKDLPEVESVNE 444
Db 405 NKTSGPILYPMNKDKWDRSSAVTP--DEEVFYLVALLRSALTGDGEETQKLEYLKDQNR 462
QY 445 KIIRFCKDSGKIKIKOYLMHYTSKEDWIEHFGSKWDDFSKRLKDLFDPKLLSPGQDIF 501
Db 463 RILEFCEQAKINVKQYLPHPHATQEEWVAHFQDKWDRFSLKAEFDPRHILATGQRIF 519
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RESULT 11
US-09-829-549A-48
; Sequence 48, Application US/09829549A
; Patent No. US20020052484A1
; GENERAL INFORMATION:
; APPLICANT: The Curators of the University of Missouri
; TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES
; FILE REFERENCE: UMO 1521.1
; CURRENT APPLICATION NUMBER: US/09/829,549A
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/195,785
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 611
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(85)
; OTHER INFORMATION: Mat-alpha secretory sequence
; NAME/KEY: DOMAIN
; LOCATION: (86)..(600)
; OTHER INFORMATION: Cytokinin oxidase 1
; NAME/KEY: DOMAIN
; LOCATION: (601)..(602)
; OTHER INFORMATION: Linker
; NAME/KEY: DOMAIN
; LOCATION: (603)..(611)
; OTHER INFORMATION: Random peptide Pc 87
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US-09-829-549A-48

Query Match      43.4%; Score 1126.5; DB 9; Length 611;
Best Local Similarity 46.8%; Pred. No. 1.1e-95;
Matches 232; Conservative 83; Mismatches 152; Indels 29; Gaps 12;

QY 30 SINLTSLTDPSSIISAASHDFGNITTTVPGGVICPSSSTADISRLLOXAANGKS--TFQVAA 87
Db 109 ALDGKLRITDSNATAAASDTDFGNITSALPAAVLYP-STGDLVALLS-AANSTPGWPYTIAP 166
QY 88 RQGHSLNGQASVSGGVIVNMTCTID-----VVVSKDKKYADVAAGTLWVDVLKKTAEK 141
Db 167 RGRGSHLMGQAFAPGVVNMASLGDAAAAPRINVSADGRYVDAGGEQVWIDVLASLAR 226
QY 142 GVSPVSWTDYHLHITVCGTSLNGGIGGVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPE 201
Db 227 GVAPRSWNDYLYLTVGGTSLNAGISGQAFHHGPOISNVLEMDVITGHGEMVTCCKQLNAD 286
QY 202 LFYGVGLGGLGQFGIITRARIIVLDHAPKRAKWFRLMYSDFTTFTTKDQERLISMANDIG--- 258
Db 287 LFDAVLGGLGQFGVITRARIAVEPAPARARWVRFVYTDFAAFSADQERLTAPRPGGGAS 346
QY 259 ---VDYLEGQIF-----LSNGVVDTSFFPPSDQSKVADLVKQHG--IYVLEVAKYVDDPN 309
Db 347 FGPMSYVEGSVFVNQSLATDLANTGFTTDADVARIVALAGERNATTVYSIEATLNYDNAT 406
QY 310 --LPIISKVIDTLTKTSLYLPFGFISMHDVAYDFLNRVHVEENKRLSLGLWELPHEWNL 367
Db 407 AAAAAVDQELASVLTSLSYVEGFQFQRDVAYAAFLDRVHGEEVALNKLGLWVPHWNLNM 466
QY 368 YVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDRMSAMIPEIDEDVYIIGL 427
Db 467 FVPRSRITADFDGRGVFKGI-LQGTDIVPLVPLNKSMMWDDGMSAATP--SEDFVYAVSL 523
QY 428 L-QSATPKDLPEVESVNEKIIRFCKDSGKIKIKOYLMHYTSKEDWIEHFG-SKWDDFSKRL 485
Db 524 LFSSVAPNDLARLQEQNRILRFCDLAGIQYKTYLARHTDRSDWVRHFGAAKWRNFVEMK 583
QY 486 DLFDPKLLSPGQDIF 501
Db 584 NKYDPKRLSPGQDIF 599
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RESULT 12
US-10-311-453-2
; Sequence 2, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-2
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Query Match      40.7%; Score 1056.5; DB 12; Length 575;
Best Local Similarity 39.8%; Pred. No. 3.3e-89;
Matches 213; Conservative 102; Mismatches 167; Indels 53; Gaps 12;
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QY 9 TLITVLMIT-----TKSSNGIKIDLPSKLNLTSLTDPSIIISAA----- 45
Db 16 TFLGIFMILVLSICIPGRNLCNSHVSSTPKELP-----SSNPSDIRSSLVSLDLEGYISFDD 72
QY 46 ----SHDFGNITTVTPGGVICPSSSTADISRLLQYAAN--GKSTFQVAARGQSHSLNGQAS 99
Db 73 VHNVAKDFGNRYQLPPLAILHPRSVDISSMMKHIVHLGSTSNLTVAAARGHSHSLNGQAL 132
QY 100 VSGGVIVNMTCI--TDVVVSKDKK-YADVAAGTLWVDVLKKTAEKGVSPVSWTDYHLHITV 156
Db 133 AHQGVVVKMESLRSPDIRYKKGQPYVDVSGGEIWINILRETLYGLSPKSWTDYHLHITV 192
QY 157 GGTLSNGGIGGVFRNGPLVSNVLELDVITGKGMELTCSRQLNPFLFYGLVGLGQFGII 216
Db 193 GGTLSNAGISGQAFKHGQPINNVYQLEIVTGKEVVTCEKRNSELFFSVLGGGQFGII 252
QY 217 TRARIVLDHAPKRAKWFRLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVD-- 274
Db 253 TRARISLEPAPHMVKWIRVLYSDFAFSRDQEYLISKEKTF--DYVEGFVIINR--TDLL 308
QY 275 ---TSFPFPPSDQSKVADLVKQHGIYVLEVAKYYDDPNLPIISKVIDTLTKTSLYLPGFI 331
Db 309 NNWRSSFSFNDSTQASRFKSDGKTLVYKFNPEEASSMDQETGKLLSELNIPSTL 368
QY 332 SMHDVAYDFLNRVHVEENKLRSLGLWELPHWPNLNVKPSRILDFHNGVVKDILLKQKS 391
Db 369 FSSEVPYIEFLDRVHIAERKLRAKGLWEVPHWPNLNLIPKSSYQFATEVFNNILTSNN- 427
QY 392 ASGLALLYPTNRNKNWDRMSAMPEIDEDEVIIYIIGLLQSATP-----KDLPEVESVNEKI 446
Db 428 -NGPILYIPVNSQKWKHTSLITP--NEDIFYLVAFLPSAVPNSSGKNDLEYLLKQNRV 484
QY 447 IRFCCKDSGKIKQYLMHYTSKEDWIEHFGSKWDDFSKRDLPKLLSPGQDIF 501
Db 485 MNFCAAANLVKQYLPHYETQKEWKSHFGKRWETFAQRKQAYDPLAILAPGORIF 539

RESULT 13
US-10-014-101-2
; Sequence 2, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-2

Query Match 40.7%; Score 1056.5; DB 14; Length 575;
Best Local Similarity 39.8%; Pred. No. 3.3e-89;
Matches 213; Conservative 102; Mismatches 167; Indels 53; Gaps 12;
QY 9 TLITVLMIT-----TKSSNGIKIDLPSKLNLTSLTDPSIIISAA----- 45
Db 16 TFLGIFMILVLSICIPGRNLCNSHVSSTPKELP---SSNPSDIRSSLVSLDLEGYISFDD 72

QY 46 ----SHDFGNITTVTPGGVICPSSSTADISRLLQYAAN--GKSTFQVAARGQSHSLNGQAS 99
Db 73 VHNVAKDFGNRYQLPPLAILHPRSVDISSMMKHIVHLGSTSNLTVAAARGHSHSLNGQAL 132
QY 100 VSGGVIVNMTCI--TDVVVSKDKK-YADVAAGTLWVDVLKKTAEKGVSPVSWTDYHLHITV 156
Db 133 AHQGVVVKMESLRSPDIRYKKGQPYVDVSGGEIWINILRETLYGLSPKSWTDYHLHITV 192
QY 157 GGTLSNGGIGGVFRNGPLVSNVLELDVITGKGMELTCSRQLNPFLFYGLVGLGQFGII 216
Db 193 GGTLSNAGISGQAFKHGQPINNVYQLEIVTGKEVVTCEKRNSELFFSVLGGGQFGII 252
QY 217 TRARIVLDHAPKRAKWFRLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVD-- 274
Db 253 TRARISLEPAPHMVKWIRVLYSDFAFSRDQEYLISKEKTF--DYVEGFVIINR--TDLL 308
QY 275 ---TSFPFPPSDQSKVADLVKQHGIYVLEVAKYYDDPNLPIISKVIDTLTKTSLYLPGFI 331
Db 309 NNWRSSFSFNDSTQASRFKSDGKTLVYKFNPEEASSMDQETGKLLSELNIPSTL 368
QY 332 SMHDVAYDFLNRVHVEENKLRSLGLWELPHWPNLNVKPSRILDFHNGVVKDILLKQKS 391
Db 369 FSSEVPYIEFLDRVHIAERKLRAKGLWEVPHWPNLNLIPKSSYQFATEVFNNILTSNN- 427
QY 392 ASGLALLYPTNRNKNWDRMSAMPEIDEDEVIIYIIGLLQSATP-----KDLPEVESVNEKI 446
Db 428 -NGPILYIPVNSQKWKHTSLITP--NEDIFYLVAFLPSAVPNSSGKNDLEYLLKQNRV 484
QY 447 IRFCCKDSGKIKQYLMHYTSKEDWIEHFGSKWDDFSKRDLPKLLSPGQDIF 501
Db 485 MNFCAAANLVKQYLPHYETQKEWKSHFGKRWETFAQRKQAYDPLAILAPGORIF 539

RESULT 14
US-10-311-453-12
; Sequence 12, Application US/103111453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-12

Query Match 38.3%; Score 993; DB 12; Length 504;
Best Local Similarity 41.5%; Pred. No. 2.2e-83;
Matches 217; Conservative 100; Mismatches 152; Indels 54; Gaps 14;
QY 6 LMITLITVLMIT-----KSSNGIKIDLPSKLNLTSLTDPSIIISAAASHDFGNITTV 55
Db 2 LIVRSFTILLSCIAFLACCFSSS-----ISSLKALPLVGHLEFEHVVHASKDFGNRYQL 57
QY 56 TPGGVICPSSSTADISRLLQ--YAANGKSTFQVAARGQSHSLNGQASVSGGVIVNMTCTID 113
Db 58 IPLAVLHPKSVSDIASTIRHIWMMGTHSOLTVAARGHSHSLNGQQAQTRHGIVIHMSLHP 117
QY 114 -----VVVSKDKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYHLHITVGGTSLNGGIGGQ 168

Db 118 QKLVYSDSPAPYVDVSGGELWINILHETLKYGLAPKSWTDYHLTVGGTSLNAGISGQ 177
QY 169 VFRNGPLVSNVLELDVITGKGMELTCSRQLNPFLFYGLGGLGQFGIITRARIIVLDHAPK 228
Db 178 AFRHGPOISNVHQLEIVTGKGEILNCTKRQNSDLFNGVLGGLGQFGIITRARIAPAP- 236
QY 229 RAKWFRMLYSDFTTFTKQERLISMANDIGVDYLEGQIFLS-NGWVDT---SFFPPSDQS 284
Db 237 -----TMDQEQQLIS-AQGHKFDYIEGFVIINRTGLNSWRLSF--TAEAP 278
QY 285 KVADLVKQHG-IIVVLEVAKYYDDPNLPILISKVIDTLTKTSLYLPGFISMHDVAYFDFLN 343
Db 279 LEASQFKFDGRTLYCLELAKYLKQDNKDVINQEVKETLSELSYVSTLTFTTEVAYEAFD 338
QY 344 RVHVEENKLSLGLWELPHPWNLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPNTR 403
Db 339 RVHVEVSKLRSKQWEVPHPWNLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPNTR 396
QY 404 NKWDNRMSAMIPEDIDEDVYIIGLLQSATP-----KD-LPEVESVNEKIIRFCKDSGKIK 458
Db 397 SKWDNQTSVATPE--EEVYLVAILTSASPGSAGKDGVEEILRRNRILEFSEAGIGLK 454
QY 459 QYLMHYTSKEDWIEHFGSKWDDFSKRKDLFDPKKLLSPGQDIF 501
Db 455 QYLPHYTTREEMRSHFGDKWGEFVRRKSRYPDLAILAPGHRIF 497

RESULT 15
US-10-014-101-12
; Sequence 12, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-12

Query Match 38.3%; Score 993; DB 14; Length 504;
Best Local Similarity 41.5%; Pred. No. 2.2e-83;
Matches 217; Conservative 100; Mismatches 152; Indels 54; Gaps 14;
QY 6 LMITLITVLMIT-----KSSNGIKIDLPKSLNLTSLTDPSSIISAASHDFGNITTV 55
Db 2 LIVRSFTILLUSCIAFKLACCFSSS-----ISSLKALPLVGHLEFEHVHASKDFGNRYQL 57
QY 56 TPGGVICPSTADISRLQ--YAANGKSTFQVAARGQCHSLNGQASVSGGVIVNMTCTID 113
Db 58 IPLAVLHPKSVSDIASTIRHIWMGTHSOLTVAARGRHSLOQQAQTRHGIVIHMESLHP 117
QY 114 -----VVVSKDKKYADVAAGTLWVDVLKKAETKGVSPVSWTDYHLITVGGTSLNGGIGGQ 168
Db 118 QKLVYSDSPAPYVDVSGGELWINILHETLKYGLAPKSWTDYHLTVGGTSLNAGISGQ 177
QY 169 VFRNGPLVSNVLELDVITGKGMELTCSRQLNPFLFYGLGGLGQFGIITRARIIVLDHAPK 228

Db 178 AFRHGPOISNVHQLEIVTGKGEILNCTKRQNSDLFNGVLGGLGQFGIITRARIAPAP- 236
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Db 237 -----TMDQEQQLIS-AQGHKFDYIEGFVIINRTGLNSWRLSF--TAEAP 278
QY 285 KVADLVKQHG-IIVVLEVAKYYDDPNLPILISKVIDTLTKTSLYLPGFISMHDVAYFDFLN 343
Db 279 LEASQFKFDGRTLYCLELAKYLKQDNKDVINQEVKETLSELSYVSTLTFTTEVAYEAFD 338
QY 344 RVHVEENKLSLGLWELPHPWNLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPNTR 403
Db 339 RVHVEVSKLRSKQWEVPHPWNLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPNTR 396
QY 404 NKWDNRMSAMIPEDIDEDVYIIGLLQSATP-----KD-LPEVESVNEKIIRFCKDSGKIK 458
Db 397 SKWDNQTSVATPE--EEVYLVAILTSASPGSAGKDGVEEILRRNRILEFSEAGIGLK 454
QY 459 QYLMHYTSKEDWIEHFGSKWDDFSKRKDLFDPKKLLSPGQDIF 501
Db 455 QYLPHYTTREEMRSHFGDKWGEFVRRKSRYPDLAILAPGHRIF 497

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